

SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Lu, Peter S.
Carman, Jonathan D.
Candia III, Albert F.
Arbbor Vita Corporation

<120> CLASP-2 TRANSMEMBRANE PROTEINS

<130> 020054-000210US

<140> US 09/687,837

<141> 2000-10-13

<150> US 60/129,171

<151> 1999-04-14

<150> US 60/134,114

<151> 1999-05-14

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<151> 2000-04-11

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Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu Leu Leu Thr Phe
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Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser Thr Lys Lys Arg
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Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys
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Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn
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Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His
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Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys
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Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu
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His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala
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cag	aag	gga	agc	acc	ctg	gac	aac	agc	ctg	cac	aag	gac	ctg	ctg	ggc	1585
Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp	Leu	Leu	Gly	
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Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	Thr	Pro	Asn	Ile	
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Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Ser	Thr	Asp	
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Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys	Ser	Asn	Ser	Leu	
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Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser	Val	Val	Arg	Cys	
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Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met	Cys	Phe	Leu	
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Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	Tyr	Trp	Asn	
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Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg	Tyr	Ile	Ala	Arg	Asn	
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Ser	Asp	Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Ile	Ala	
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act	gag	gtt	tgc	ctg	aca	gct	ctg	gac	acg	ctt	tct	cta	ttt	aca	ttg	2209
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	aaa aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa cat cag tct Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser			2305
	755	760	765	
	gaa acg gct tta aaa aat gtc ttc act gcc tta agg tcc tta att tat Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr			2353
	770	775	780	
	aag ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg tgt gcg gct Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala			2401
	785	790	795	800
	ctg tgt tac gag att ctc aag tgc tgt aac tcc aag ctg agc tcc atc Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile			2449
	805	810	815	
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	820	825	830	
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	835	840	845	
	ata tct gtc agc cag ctg ata gca gac gtt gtt ggc att ggg gaa acc Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu Thr			2593
	850	855	860	
	aga ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc aac agt gac Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp			2641
	865	870	875	880
	cgg ctt att aag cac acc agc ttc tcc tct gat gtg aag gac tta acc Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr			2689
	885	890	895	
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	900	905	910	
	gag aac gac cca gag atg ctg gtg gac ctc cag tac agc ctg gcc aaa Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys			2785
	915	920	925	
	tcc tat gcc agc acg ccc gag ctc agg aag acg tgg ctc gac agc atg Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met			2833
	930	935	940	
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	tat gtc cac gta aca gcc cta gtg gca gaa tat ctc aca cgg aaa ggc Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Gly			2929
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Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr	
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agt aag aag gtg gcg gag ctc cgg cag ctg tgc tcc tcg gcc gag gtg	3649
Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val	
1205 1210 1215	

Q26
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 (CLASP-2A)

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 35 40 45
 Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys
 50 55 60
 Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn
 65 70 75 80
 Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His
 85 90 95
 Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys
 100 105 110
 Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu
 115 120 125
 His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala
 130 135 140
 Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu
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 Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe
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 Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr
 180 185 190
 Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu
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 Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr
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 Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met
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 Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile Ser Cys
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 Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe Glu Phe
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 Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro
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 385 390 395 400
 Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu Val Gly

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a26
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Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val	
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Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu	
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Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala	
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Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr	
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Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser	
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Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys	
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Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val	
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Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr	
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Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu	
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Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile	
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Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg	
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Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val	
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Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr	
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Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser	
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Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val	
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a26
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Cys	Phe	Leu	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	
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Gln	Thr	Leu	Pro	Val	Ser	Arg	Asn	Arg	Thr	Gly	Met	Met	His	Ala	Arg	
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Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu	
1185 1190 1195 1200	
aag acg agc gtc tta ccg aat tcc ctt cac atc ttc aac gcc atc agt	3648
Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala Ile Ser	
1205 1210 1215	
ggg act cca aca agc aca atg gtt cac ggg atg acc agc tcg tct tcg	3696
Gly Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser Ser Ser	
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Val Val	

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 <223> Human cadherin-like asymmetry protein 2B
 (CLASP-2B)

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 Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu
 35 40 45
 Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala
 50 55 60
 Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr
 65 70 75 80
 Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser
 85 90 95
 Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys
 100 105 110
 Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg
 115 120 125
 Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val
 130 135 140
 Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu
 145 150 155 160
 Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys
 165 170 175

Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr
 180 185 190
 Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys
 195 200 205
 Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu
 210 215 220
 Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp
 225 230 235 240
 Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe
 245 250 255
 Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe
 260 265 270
 Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile
 275 280 285
 Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg
 290 295 300
 Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val
 305 310 315 320
 Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly
 325 330 335
 Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu
 340 345 350
 Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp
 355 360 365
 Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr
 370 375 380
 Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile
 385 390 395 400
 Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser
 405 410 415
 Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val
 420 425 430
 Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met
 435 440 445
 Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr
 450 455 460
 Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile
 465 470 475 480
 Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile
 485 490 495

Ala	Arg	Asn	Gln	Glu	Gly	Leu	Gly	Pro	Ile	Val	His	Asp	Arg	Lys	Ser			
			500					505					510					
Gln	Thr	Leu	Pro	Val	Ser	Arg	Asn	Arg	Thr	Gly	Met	Met	His	Ala	Arg			
		515					520					525						
Leu	Gln	Gln	Leu	Gly	Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser			
		530				535					540							
Tyr	Gly	His	Ser	Asp	Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala			
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Asn	Ile	Ala	Thr	Glu	Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu			
				565					570					575				
Phe	Thr	Leu	Ala	Phe	Lys	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	Leu			
			580					585					590					
Met	Lys	Lys	Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His	Gln			
		595					600					605						
Ser	Glu	Thr	Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser	Leu	Ile			
		610				615					620							
Tyr	Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala			
625					630					635					640			
Ala	Leu	Cys	Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser			
				645					650					655				
Ile	Arg	Thr	Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn			
			660					665					670					
Phe	Asp	Tyr	Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val			
		675					680					685						
Ile	Ile	Ser	Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Val	Gly	Ile	Gly	Glu			
		690				695					700							
Thr	Arg	Phe	Gln	Gln	Ser	Leu	Ser	Ile	Ile	Asn	Asn	Cys	Ala	Asn	Ser			
705					710					715					720			
Asp	Arg	Leu	Ile	Lys	His	Thr	Ser	Phe	Ser	Ser	Asp	Val	Lys	Asp	Leu			
				725				730					735					
Thr	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu			
			740					745					750					
His	Glu	Asn	Asp	Pro	Glu	Met	Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	Ala			
		755					760					765						
Lys	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser			
		770				775					780							
Met	Ala	Arg	Ile	His	Val	Lys	Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met			
785					790					795					800			
Cys	Tyr	Val	His	Val	Thr	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys			
				805					810					815				
Gly	Val	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile	Thr	Pro	Asn			

all
cont.

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Ile	Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Met	Gln	Asp	Val		
835						840						845					
His	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln	Cys	Ala	Asp		
850						855						860					
Gly	Leu	Trp	Lys	Ala	Glu	Arg	Tyr	Glu	Leu	Ile	Ala	Asp	Ile	Tyr	Lys		
865						870						875					
Leu	Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe	Glu	Arg	Leu	Ala		
885						890						895					
His	Leu	Tyr	Asp	Thr	Leu	His	Arg	Ala	Tyr	Ser	Lys	Val	Thr	Glu	Val		
900						905						910					
Met	His	Ser	Gly	Arg	Arg	Leu	Leu	Gly	Thr	Tyr	Phe	Arg	Val	Ala	Phe		
915						920						925					
Phe	Gly	Gln	Gly	Phe	Phe	Glu	Asp	Glu	Asp	Gly	Lys	Glu	Tyr	Ile	Tyr		
930						935						940					
Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	Ile	Ser	Gln	Arg	Leu	Leu		
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Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	Asn	Val	Lys	Met	Ile	Gln		
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Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	Asp	Ser	Lys	Tyr	Ala	Tyr		
980						985						990					
Ile	Gln	Val	Thr	His	Val	Ile	Pro	Phe	Phe	Asp	Glu	Lys	Glu	Leu	Gln		
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Glu	Arg	Lys	Thr	Glu	Phe	Glu	Arg	Ser	His	Asn	Ile	Arg	Arg	Phe	Met		
1010						1015						1020					
Phe	Glu	Met	Pro	Phe	Thr	Gln	Thr	Gly	Lys	Arg	Gln	Gly	Gly	Val	Glu		
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Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	Ala	Ile	His	Cys	Phe	Pro		
1045						1050						1055					
Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	Tyr	Gln	His	His	Thr	Asp	Leu		
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Asn	Pro	Ile	Glu	Val	Ala	Ile	Asp	Glu	Met	Ser	Lys	Lys	Val	Ala	Glu		
1075						1080						1085					
Leu	Arg	Gln	Leu	Cys	Ser	Ser	Ala	Glu	Val	Asp	Met	Ile	Lys	Leu	Gln		
1090						1095						1100					
Leu	Lys	Leu	Gln	Gly	Ser	Val	Ser	Val	Gln	Val	Asn	Ala	Gly	Pro	Leu		
1105						1110						1115					
Ala	Tyr	Ala	Arg	Ala	Phe	Leu	Asp	Asp	Thr	Asn	Thr	Lys	Arg	Tyr	Pro		
1125						1130						1135					
Asp	Asn	Lys	Val	Lys	Leu	Leu	Lys	Glu	Val	Phe	Arg	Gln	Phe	Val	Glu		
1140						1145						1150					

Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys Glu Asp
1155 1160 1165

Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu Met Ala
1170 1175 1180

Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu
1185 1190 1195 1200

Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala Ile Ser
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Gly Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser Ser Ser
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Val Val

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(CLASP-2C)

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gag gag gcc tcc atg atg gaa gac gtg ggg atg cag gat gtc cat ttc 97
Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His Phe
20 25 30

aac gag gat gtg ctg atg gag ctc ctt gag cag tgc gca gat gga ctc 145
Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu
35 40 45

tgg aaa gcc gag cgc tac gag ctc atc gcc gac atc tac aaa ctt atc 193
Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile
50 55 60

atc ccc att tat gag aag cgg agg gat ttt gag agg ctg gcc cat ctg 241
Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu
65 70 75 80

tat gac acg ctg cac cgg gcc tac agc aaa gtg acc gag gtc atg cac 289
Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His
85 90 95

tcg ggc cgc agg ctt ctg ggg acc tac ttc cgg gta gcc ttc ttc ggg 337
Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe Gly

100	105	110	
cag gga ttc ttt gaa gat gaa gat gga aag gag tat att tac aag gaa			385
Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu			
115	120	125	
ccc aaa ctc aca ccg ctg tcg gaa att tct cag aga ctc ctt aaa ctg			433
Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu			
130	135	140	
tac tcg gat aaa ttt ggt tct gaa aat gtc aaa atg aca cag gat tct			481
Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser			
145	150	155	160
ggc aag gtc aac cct aag gat ctg gat tct aag tat gca tac atc cag			529
Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln			
165	170	175	
gtg act cac gtc atc ccc ttc ttt gac gaa aaa gag ttg caa gaa agg			577
Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg			
180	185	190	
aaa aca gag ttt gag aga tcc cac aac atc cgc cgc ttc atg ttt gag			625
Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu			
195	200	205	
atg cca ttt acg cag acc ggg aag agg cag ggc ggg gtg gaa gag cag			673
Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln			
210	215	220	
tgc aaa cgg cgc acc atc ctg aca gcc ata cac tgc ttc cct tat gtg			721
Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val			
225	230	235	240
aag aag cgc atc cct ttc atg tac cag cac cac act gac ctg aac ccc			769
Lys Lys Arg Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro			
245	250	255	
atc gag gtc cat tga cgagatgagt aagaagggtgg cggagctccg gcagctgtgc			824
Ile Glu Val His			
260			
tcctcggccg aggtggacat gatcaaactg cagctcaaac tccagggcag cgtgagtgtt			884
caggtcaatg ctggcccact agcatatgcg cgagctttct tagatgatac aaacacaaag			944
cgatatcctg acaataaagt gaagctgctt aaggaagttt tcaggcaatt tgtggaagct			1004
tgcggtcaag ccttagcggc aaacgaacgt ctgattaaag aagaccagct cgagtatcag			1064
gaagaaatga aagccaacta cagggaaatg gcgaaggagc tttctgaaat catgcatgag			1124
cagatctgcc ccctggagga gaagacgagc gtcttaccga attcccttca catcttcaac			1184
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gtgtga			1250

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 (CLASP-2C)

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 20 25 30
 Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu
 35 40 45
 Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile
 50 55 60
 Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu
 65 70 75 80
 Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His
 85 90 95
 Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe Gly
 100 105 110
 Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu
 115 120 125
 Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
 130 135 140
 Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
 145 150 155 160
 Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
 165 170 175
 Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg
 180 185 190
 Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu
 195 200 205
 Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln
 210 215 220
 Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val
 225 230 235 240
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 Ile Glu Val His
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 (CLASP-2D) KIAA1058

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caa gac agc aat aag cta tcc aat gat gac atg ctc aag tta ctt gca	96
Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala	
20 25 30	
gac ttt cgg aaa cct gag aag atg gct aag ctc cca gtg att tta ggc	144
Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly	
35 40 45	
aat cta gac att aca att gat aat gtt tcc tca gac ttc cct aat tat	192
Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr	
50 55 60	
gtt aat tca tca tac att ccc aca aaa caa ttt gaa acc tgc agt aaa	240
Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys	
65 70 75 80	
act ccc atc acg ttt gaa gtg gag gaa ttt gtg ccc tgc ata cca aaa	288
Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys	
85 90 95	
cac act cag cct tac acc atc tac acc aat cac ctt tac gtt tat cct	336
His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro	
100 105 110	
aag tac ttg aaa tac gac agt cag aag tct ttt gcc aag gct aga aat	384
Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn	
115 120 125	
att gcg att tgc att gaa ttc aaa gat tca gat gag gaa gac tct cag	432
Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln	
130 135 140	
ccc ctt aag tgc att tat ggc aga cct ggt ggg cca gtt ttc aca aga	480
Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg	
145 150 155 160	
agc gcc ttt gct gca gtt tta cac cat cac caa aac cca gaa ttt tat	528
Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr	
165 170 175	
gat gag att aaa ata gag ttg ccc act cag ctg cat gaa aag cac cac	576
Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His	
180 185 190	
ctg ttg ctc aca ttc ttc cat gtc agc tgt gac aac tca agt aaa gga	624
Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly	
195 200 205	
agc acg aag aag agg gat gtc gtt gaa acc caa gtt ggc tac tcc tgg	672
Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp	
210 215 220	
ctt ccc ctc ctg aaa gac gga agg gtg gtg aca agc gag cag cac atc	720
Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile	
225 230 235 240	
ccg gtc tcg gcg aac ctt cct tcg ggc tat ctt ggc tac cag gag ctt	768
Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu	
245 250 255	
ggg atg ggc agg cat tat ggt ccg gaa att aaa tgg gta gat gga ggc	816

Q26
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Gly	Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	
			260					265					270			
aag	cca	ctg	ctg	aaa	att	tcc	act	cat	ctg	gtt	tct	aca	gtg	tat	act	864
Lys	Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	
		275					280					285				
cag	gat	cag	cat	tta	cat	aat	ttt	ttc	cag	tac	tgt	cag	aaa	acc	gaa	912
Gln	Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	
	290					295					300					
tct	gga	gcc	caa	gcc	tta	gga	aac	gaa	ctt	gta	aag	tac	ctt	aag	agt	960
Ser	Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	
305					310					315					320	
ctg	cat	gcg	atg	gaa	ggc	cac	gtg	atg	atc	gcc	ttc	ttg	ccc	act	atc	1008
Leu	His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	
				325					330					335		
cta	aac	cag	ctg	ttc	cga	gtc	ctc	acc	aga	gcc	aca	cag	gaa	gaa	gtc	1056
Leu	Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	
			340					345					350			
gcg	gtt	aac	gtg	act	cgg	gtc	att	att	cat	gtg	gtt	gcc	cag	tgc	cat	1104
Ala	Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	
		355					360					365				
gag	gaa	gga	ttg	gag	agc	cac	ttg	agg	tca	tat	gtt	aag	tac	gcg	tat	1152
Glu	Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	
	370					375					380					
aag	gct	gag	cca	tat	gtt	gcc	tct	gaa	tac	aag	aca	gtg	cat	gaa	gaa	1200
Lys	Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	
385					390					395					400	
ctg	acc	aaa	tcc	atg	acc	acg	att	ctc	aag	cct	tct	gcc	gat	ttc	ctc	1248
Leu	Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	
				405					410					415		
acc	agc	aac	aaa	cta	ctg	aag	tac	tca	tgg	ttt	ttc	ttt	gat	gta	ctg	1296
Thr	Ser	Asn	Lys	Leu	Leu	Lys	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	
			420					425					430			
atc	aaa	tct	atg	gct	cag	cat	ttg	ata	gag	aac	tcc	aaa	gtt	aag	ttg	1344
Ile	Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	
		435					440					445				
ctg	cga	aac	cag	aga	ttt	cct	gca	tcc	tat	cat	cat	gca	gtg	gaa	acc	1392
Leu	Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Val	Glu	Thr	
	450					455						460				
gtt	gta	aat	atg	ctg	atg	cca	cac	atc	act	cag	aag	ttt	cga	gat	aat	1440
Val	Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Arg	Asp	Asn	
465					470					475					480	
cca	gag	gca	tct	aag	aac	gcg	aat	cat	agc	ctt	gct	gtc	ttc	atc	aag	1488
Pro	Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	
				485					490					495		
aga	tgt	ttc	acc	ttc	atg	gac	agg	ggc	ttt	gtc	ttc	aag	cag	atc	aac	1536
Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	

Q26
cont.

500						505						510						
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Asn	Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu			
		515					520					525						
tac	aag	ttt	gaa	ttt	ctc	cgt	gta	gtg	tgc	aac	cat	gaa	cat	tat	att	1632		
Tyr	Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile			
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ccg	ttg	aac	tta	cca	atg	cca	ttt	gga	aaa	ggc	agg	att	caa	aga	tac	1680		
Pro	Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr			
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caa	gac	ctc	cag	ctt	gac	tac	tca	tta	aca	gat	gag	ttc	tgc	aga	aac	1728		
Gln	Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn			
				565					570					575				
cac	ttc	ttg	gtg	gga	ctg	tta	ctg	agg	gag	gtg	ggg	aca	gcc	ctc	cag	1776		
His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln			
			580					585					590					
gag	ttc	cgg	gag	gtc	cgt	ctg	atc	gcc	atc	agt	gtg	ctc	aag	aac	ctg	1824		
Glu	Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu			
		595					600					605						
ctg	ata	aag	cat	tct	ttt	gat	gac	aga	tat	gct	tca	agg	agc	cat	cag	1872		
Leu	Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln			
	610					615					620							
gca	agg	ata	gcc	acc	ctc	tac	ctg	cct	ctg	ttt	ggc	ctg	ctg	att	gaa	1920		
Ala	Arg	Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu			
625					630					635					640			
aac	gtc	cag	cgg	atc	aat	gtg	agg	gat	gtg	tca	ccc	ttc	cct	gtg	aac	1968		
Asn	Val	Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn			
				645					650					655				
gcg	ggc	atg	act	gtg	aag	gat	gaa	tcc	ctg	gct	cta	cca	gct	gtg	aat	2016		
Ala	Gly	Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn			
			660					665					670					
ccg	ctg	gtg	acg	ccg	cag	aag	gga	agc	acc	ctg	gac	aac	agc	ctg	cac	2064		
Pro	Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His			
		675					680					685						
aag	gac	ctg	ctg	ggc	gcc	atc	tcc	ggc	att	gct	tct	cca	tat	aca	acc	2112		
Lys	Asp	Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr			
	690					695					700							
tca	act	cca	aac	atc	aac	agt	gtg	aga	aat	gct	gat	tcg	aga	gga	tct	2160		
Ser	Thr	Pro	Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser			
705					710					715					720			
ctc	ata	agc	aca	gat	tcg	ggc	aac	agc	ctt	cca	gaa	agg	aat	agt	gag	2208		
Leu	Ile	Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu			
				725					730					735				
aag	agc	aat	tcc	ctg	gat	aag	cac	caa	caa	agt	agc	aca	ttg	gga	aat	2256		
Lys	Ser	Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn			
			740					745					750					

all
cont.

tcc	gtg	gtt	cgc	tgt	gat	aaa	ctt	gac	cag	tct	gag	att	aag	agc	cta	2304
Ser	Val	Val	Arg	Cys	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	
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ctg	atg	tgt	ttc	ctc	tac	atc	tta	aag	agc	atg	tct	gat	gat	gct	ttg	2352
Leu	Met	Cys	Phe	Leu	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	
	770					775					780					
ttt	aca	tat	tgg	aac	aag	gct	tca	aca	tct	gaa	ctt	atg	gat	ttt	ttt	2400
Phe	Thr	Tyr	Trp	Asn	Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	
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Thr	Ile	Ser	Glu	Val	Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg	
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tac	ata	gcc	aga	aca	gga	atg	atg	cat	gcc	aga	ttg	cag	cag	ctg	ggc	2496
Tyr	Ile	Ala	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	Gln	Gln	Leu	Gly	
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agc	ctg	gat	aac	tct	ctc	act	ttt	aac	cac	agc	tat	ggc	cac	tcg	gac	2544
Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser	Tyr	Gly	His	Ser	Asp	
		835					840					845				
gca	gat	gtt	ctg	cac	cag	tca	tta	ctt	gaa	gcc	aac	att	gct	act	gag	2592
Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Ile	Ala	Thr	Glu	
	850					855					860					
gtt	tgc	ctg	aca	gct	ctg	gac	acg	ctt	tct	cta	ttt	aca	ttg	gcg	ttt	2640
Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu	Phe	Thr	Leu	Ala	Phe	
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aag	aac	cag	ctc	ctg	gcc	gac	cat	gga	cat	aat	cct	ctc	atg	aaa	aaa	2688
Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	Leu	Met	Lys	Lys	
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gtt	ttt	gat	gtc	tac	ctg	tgt	ttt	ctt	caa	aaa	cat	cag	tct	gaa	acg	2736
Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His	Gln	Ser	Glu	Thr	
			900					905					910			
gct	tta	aaa	aat	gtc	ttc	act	gcc	tta	agg	tcc	tta	att	tat	aag	ttt	2784
Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser	Leu	Ile	Tyr	Lys	Phe	
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ccc	tca	aca	ttc	tat	gaa	ggg	aga	gcg	gac	atg	tgt	gcg	gct	ctg	tgt	2832
Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala	Ala	Leu	Cys	
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tac	gag	att	ctc	aag	tgc	tgt	aac	tcc	aag	ctg	agc	tcc	atc	agg	acg	2880
Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser	Ile	Arg	Thr	
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gag	gcc	tcc	cag	ctg	ctc	tac	ttc	ctg	atg	agg	aac	aac	ttt	gat	tac	2928
Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn	Phe	Asp	Tyr	
				965				970						975		
act	gga	aag	aag	tcc	ttt	gtc	cgg	aca	cat	ttg	caa	gtc	atc	ata	tct	2976
Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val	Ile	Ile	Ser	
			980					985					990			

a26
m

gtc agc cag ctg ata gca gac gtt gtt ggc att ggg gga acc aga ttc	3024
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe	
995 1000 1005	
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Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu	
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Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg	
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Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn	
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Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr	
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Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg	
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Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val	
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cac gta aca gcc cta gtg gca gaa tat ctc aca cgg aaa gaa gca gtc	3360
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val	
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Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg	
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Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val	
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Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly	
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atg cag gat gtc cat ttc aac gag gat gtg ctg atg gag ctc ctt gag	3552
Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu	
1170 1175 1180	
cag tgc gca gat gga ctc tgg aaa gcc gag cgc tac gag ctc att gcc	3600
Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala	
1185 1190 1195 1200	
gac atc tac aaa ctt atc atc ccc att tat gag aag cgg agg gat ttt	3648
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Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys	
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gtg acc gag gtc atg cac tcg ggc cgc agg ctt ctg ggg acc tac ttc	3744

Q20
cut

Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe	
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cgg gta gcc ttc ttc ggg cag gca gcg caa tac cag ttt aca gac agt	3792
Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser	
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1265 1270 1275 1280	
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Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met	
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ata cag gat tct ggc aag gtc aac cct aag gat ctg gat tct aag tat	3984
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Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu	
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ttg caa gaa agg aaa aca gag ttt gag aga tcc cac aac atc cgc cgc	4080
Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg	
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ttc atg ttt gag atg cca ttt acg cag acc ggg aag agg cag ggc ggg	4128
Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly	
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gtg gaa gag cag tgc aaa cgg cgc acc atc ctg aca gcc ata cac tgc	4176
Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys	
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Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr	
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Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val	
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Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys	
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ctg cag ctc aaa ctc cag ggc agc gtg agt gtt cag gtc aat gct ggc	4368
Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly	
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Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg	
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Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe	

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Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys			
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Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu			
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Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Leu Gly			
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(CLASP-2D) KIAA1058

<400> 8

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Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
20 25 30

Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
35 40 45

Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
50 55 60

Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
65 70 75 80

Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
85 90 95

His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
100 105 110

Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
115 120 125

Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
130 135 140

Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
145 150 155 160

Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
165 170 175

Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
180 185 190

Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly
195 200 205

Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp
210 215 220

Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile
225 230 235 240

Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu
245 250 255

Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly
260 265 270

Lys Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr
275 280 285

Gln Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu
290 295 300

Ser Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser
 305 310 315 320
 Leu His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile
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 Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val
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 Ala Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His
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 Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu
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 Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Val Glu Thr
 450 455 460
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 Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys
 485 490 495
 Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn
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 His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln
 580 585 590
 Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu
 595 600 605
 Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln
 610 615 620
 Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu

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Ala Gly Met Thr Val	Lys Asp Glu Ser Leu	Ala Leu Pro Ala Val	Asn			
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Pro Leu Val Thr Pro	Gln Lys Gly Ser Thr	Leu Asp Asn Ser Leu	His			
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	690		695			700
Ser Thr Pro Asn Ile	Asn Ser Val Arg Asn	Ala Asp Ser Arg Gly	Ser			
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Leu Ile Ser Thr Asp	Ser Gly Asn Ser Leu	Pro Glu Arg Asn Ser	Glu			
	725		730			735
Lys Ser Asn Ser Leu	Asp Lys His Gln Gln	Ser Ser Thr Leu Gly	Asn			
	740		745			750
Ser Val Val Arg Cys	Asp Lys Leu Asp Gln	Ser Glu Ile Lys Ser	Leu			
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Leu Met Cys Phe Leu	Tyr Ile Leu Lys Ser	Met Ser Asp Asp Ala	Leu			
	770		775			780
Phe Thr Tyr Trp Asn	Lys Ala Ser Thr Ser	Glu Leu Met Asp Phe	Phe			
	785		790			795
Thr Ile Ser Glu Val	Cys Leu His Gln Phe	Gln Tyr Met Gly Lys	Arg			
	805		810			815
Tyr Ile Ala Arg Thr	Gly Met Met His Ala	Arg Leu Gln Gln Leu	Gly			
	820		825			830
Ser Leu Asp Asn Ser	Leu Thr Phe Asn His	Ser Tyr Gly His Ser	Asp			
	835		840			845
Ala Asp Val Leu His	Gln Ser Leu Leu Glu	Ala Asn Ile Ala Thr	Glu			
	850		855			860
Val Cys Leu Thr Ala	Leu Asp Thr Leu Ser	Leu Phe Thr Leu Ala	Phe			
	865		870			875
Lys Asn Gln Leu Leu	Ala Asp His Gly His	Asn Pro Leu Met Lys	Lys			
	885		890			895
Val Phe Asp Val Tyr	Leu Cys Phe Leu Gln	Lys His Gln Ser Glu	Thr			
	900		905			910
Ala Leu Lys Asn Val	Phe Thr Ala Leu Arg	Ser Leu Ile Tyr Lys	Phe			
	915		920			925
Pro Ser Thr Phe Tyr	Glu Gly Arg Ala Asp	Met Cys Ala Ala Leu	Cys			
	930		935			940
Tyr Glu Ile Leu Lys	Cys Cys Asn Ser Lys	Leu Ser Ser Ile Arg	Thr			
	945		950			955
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Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
 965 970 975
 Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
 980 985 990
 Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
 995 1000 1005
 Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
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 Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
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 Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
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 Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
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 Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
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 His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
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 Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
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 Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
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 Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
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Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
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 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
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 Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
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 Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
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 Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
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 Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
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 Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
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 Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
 1395 1400 1405
 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
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 Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
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 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
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 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
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 Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
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 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
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2E)

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cag ctg ttc cga gtc ctc acc aga gcc aca cag gaa gaa gtc gcg gtt	96
Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val	
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aac gtg act cgg gtc att att cat gtg gtt gcc cag tgc cat gag gaa	144
Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu	
35 40 45	
gga ttg gag agc cac ttg agg tca tat gtt aag tac gcg tat aag gct	192
Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala	
50 55 60	
gag cca tat gtt gcc tct gaa tac aag aca gtg cat gaa gaa ctg acc	240
Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr	
65 70 75 80	
aaa tcc atg acc acg att ctc aag cct tct gcc gat ttc ctc acc agc	288
Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser	
85 90 95	
aac aaa cta ctg agg tac tca tgg ttt ttc ttt gat gta ctg atc aaa	336
Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys	
100 105 110	
tct atg gct cag cat ttg ata gag aac tcc aaa gtt aag ttg ctg cga	384
Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg	
115 120 125	
aac cag aga ttt cct gca tcc tat cat cat gca gcg gaa acc gtt gta	432
Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val	
130 135 140	
aat atg ctg atg cca cac atc act cag aag ttt gga gat aat cca gag	480
Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu	
145 150 155 160	
gca tct aag aac gcg aat cat agc ctt gct gtc ttc atc aag aga tgt	528
Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys	
165 170 175	
ttc acc ttc atg gac agg ggc ttt gtc ttc aag cag atc aac aac tac	576
Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr	
180 185 190	
att agc tgt ttt gct cct gga gac cca aag acc ctc ttt gaa tac aag	624
Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys	
195 200 205	
ttt gaa ttt ctc cgt gta gtg tgc aac cat gaa cat tat att ccg ttg	672
Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu	
210 215 220	
aac tta cca atg cca ttt gga aaa ggc agg att caa aga tac caa gac	720
Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp	

Q26
cont.

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Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	Phe	
				245					250					255		
ttg	gtg	gga	ctg	tta	ctg	agg	gag	gtg	ggg	aca	gcc	ctc	cag	gag	ttc	816
Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	Phe	
			260					265					270			
cgg	gag	gtc	cgt	ctg	atc	gcc	atc	agt	gtg	ctc	aag	aac	ctg	ctg	ata	864
Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	Ile	
		275					280					285				
aag	cat	tct	ttt	gat	gac	aga	tat	gct	tca	agg	agc	cat	cag	gca	agg	912
Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	Arg	
	290					295					300					
ata	gcc	acc	ctc	tac	ctg	cct	ctg	ttt	ggg	ctg	ctg	att	gaa	aac	gtc	960
Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	Val	
305					310				315						320	
cag	cgg	atc	aat	gtg	agg	gat	gtg	tca	ccc	ttc	cct	gtg	aac	gcg	ggc	1008
Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	Gly	
				325				330						335		
atg	acc	gtg	aag	gat	gaa	tcc	ctg	gct	cta	cca	gct	gtg	aat	ccg	ctg	1056
Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	Leu	
			340					345					350			
gtg	acg	ccg	cag	aag	gga	agc	acc	ctg	gac	aac	agc	ctg	cac	aag	gac	1104
Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp	
		355					360					365				
ctg	ctg	ggc	gcc	atc	tcc	ggc	att	gct	tct	cca	tat	aca	acc	tca	act	1152
Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	Thr	
	370					375					380					
cca	aac	atc	aac	agt	gtg	aga	aat	gct	gat	tcg	aga	gga	tct	ctc	ata	1200
Pro	Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile	
385					390					395					400	
agc	aca	gat	tcg	ggg	aac	agc	ctt	cca	gaa	agg	aat	agt	gag	aag	agc	1248
Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys	Ser	
				405					410					415		
aat	tcc	ctg	gat	aag	cac	caa	caa	agt	agc	aca	ttg	gga	aat	tcc	gtg	1296
Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser	Val	
			420					425					430			
gtt	cgc	tgt	gat	aaa	ctt	gac	cag	tct	gag	att	aag	agc	cta	ctg	atg	1344
Val	Arg	Cys	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met	
		435					440					445				
tgt	ttc	ctc	tac	atc	tta	aag	agc	atg	tct	gat	gat	gct	ttg	ttt	aca	1392
Cys	Phe	Leu	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	
	450					455					460					
tat	tgg	aac	aag	gct	tca	aca	tct	gaa	ctt	atg	gat	ttt	ttt	aca	ata	1440
Tyr	Trp	Asn	Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	Thr	Ile	
465					470					475					480	

a26
ent.

tct gaa gtc tgc ctg cac cag ttc cag tac atg ggg aag cga tac ata	1488
Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile	
485 490 495	
gcc agg aac cag gag ggg ttg gga ccc ata gtt cat gat cga aag tct	1536
Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser	
500 505 510	
cag aca ttg cct gtt tcc cgt aac aga aca gga atg atg cat gcc aga	1584
Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg	
515 520 525	
ttg cag cag ctg ggc agc ctg gat aac tct ctc act ttt aac cac agc	1632
Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser	
530 535 540	
tat ggc cac tcg gac gca gat gtt ctg cac cag tca tta ctt gaa gcc	1680
Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala	
545 550 555 560	
aac att gct act gag gtt tgc ctg aca gct ctg gac acg ctt tct cta	1728
Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu	
565 570 575	
ttt aca ttg gcg ttt aag aac cag ctc ctg gcc gac cat gga cat aat	1776
Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn	
580 585 590	
cct ctc atg aaa aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa	1824
Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys	
595 600 605	
cat cag tct gaa acg gct tta aaa aat gtc ttc act gcc tta agg tcc	1872
His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser	
610 615 620	
tta att tat aag ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg	1920
Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met	
625 630 635 640	
tgt gcg gct ctg tgt tac gag att ctc aag tgc tgt aac tcc aag ctg	1968
Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu	
645 650 655	
agc tcc atc agg acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg	2016
Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg	
660 665 670	
aac aac ttt gat tac act gga aag aag tcc ttt gtc cgg aca cat ttg	2064
Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu	
675 680 685	
caa gtc atc ata tct gtc agc cag ctg ata gca gac gtt gtt ggc att	2112
Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile	
690 695 700	
ggg gaa acc aga ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc	2160
Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala	
705 710 715 720	

Q26
ent.

aac agt gac cgg ctt att aag cac acc agc ttc tcc tct gat gtg aag	2208
Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys	
725 730 735	
gac tta acc aaa agg ata cgc acg gtg cta atg gcc acc gcc cag atg	2256
Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met	
740 745 750	
aag gag cat gag aac gac cca gag atg ctg gtg gac ctc cag tac agc	2304
Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser	
755 760 765	
ctg gcc aaa tcc tat gcc agc acg ccc gag ctc agg aag acg tgg ctc	2352
Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu	
770 775 780	
gac agc atg gcc agg atc cat gtc aaa aat ggc gat ctc tca gag gca	2400
Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala	
785 790 795 800	
gca atg tgc tat gtc cac gta aca gcc cta gtg gca gaa tat ctc aca	2448
Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr	
805 810 815	
cgg aaa ggc gtg ttt aga caa gga tgc acc gcc ttc agg gtc att acc	2496
Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr	
820 825 830	
cca aac atc gac gag gag gcc tcc atg atg gaa gac gtg ggg aaa gcc	2544
Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Lys Ala	
835 840 845	
gag cgc tac gag ctc atc gcc gac atc tac aaa ctt atc atc ccc att	2592
Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile Ile Pro Ile	
850 855 860	
tat gag aag cgg agg gat ttt gag agg ctg gcc cat ctg tat gac acg	2640
Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu Tyr Asp Thr	
865 870 875 880	
ctg cac cgg gcc tac agc aaa gtg acc gag gtc atg cac tcg ggc cgc	2688
Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His Ser Gly Arg	
885 890 895	
agg ctt ctg ggg acc tac ttc cgg gta gcc ttc ttc ggg cag gga ttc	2736
Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe Gly Gln Gly Phe	
900 905 910	
ttt gaa gat gaa gat gga aag gag tat att tac aag gaa ccc aaa ctc	2784
Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu	
915 920 925	
aca ccg ctg tcg gaa att tct cag aga ctc ctt aaa ctg tac tcg gat	2832
Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp	
930 935 940	
aaa ttt ggt tct gaa aat gtc aaa atg ata cag gat tct ggc aag gtc	2880
Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val	
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Q26
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				965					970					975		
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Val	Ile	Pro	Phe	Phe	Asp	Glu	Lys	Glu	Leu	Gln	Glu	Arg	Lys	Thr	Glu	
			980					985					990			
ttt	gag	aga	tcc	cac	aac	atc	cgc	cgc	ttc	atg	ttt	gag	atg	cca	ttt	3024
Phe	Glu	Arg	Ser	His	Asn	Ile	Arg	Arg	Phe	Met	Phe	Glu	Met	Pro	Phe	
		995					1000					1005				
acg	cag	acc	ggg	aag	agg	cag	ggc	ggg	gtg	gaa	gag	cag	tgc	aaa	cgg	3072
Thr	Gln	Thr	Gly	Lys	Arg	Gln	Gly	Gly	Val	Glu	Glu	Gln	Cys	Lys	Arg	
	1010					1015					1020					
cgc	acc	atc	ctg	aca	gcc	ata	cac	tgc	ttc	cct	tat	gtg	aag	aag	cgc	3120
Arg	Thr	Ile	Leu	Thr	Ala	Ile	His	Cys	Phe	Pro	Tyr	Val	Lys	Lys	Arg	
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atc	cct	gtc	atg	tac	cag	cac	cac	act	gac	ctg	aac	ccc	atc	gag	gtg	3168
Ile	Pro	Val	Met	Tyr	Gln	His	His	Thr	Asp	Leu	Asn	Pro	Ile	Glu	Val	
				1045				1050					1055			
gcc	att	gac	gag	atg	agt	aag	aag	gtg	gcg	gag	ctc	cgg	cag	ctg	tgc	3216
Ala	Ile	Asp	Glu	Met	Ser	Lys	Lys	Val	Ala	Glu	Leu	Arg	Gln	Leu	Cys	
		1060					1065					1070				
tcc	tcg	gcc	gag	gtg	gac	atg	atc	aaa	ctg	cag	ctc	aaa	ctc	cag	ggc	3264
Ser	Ser	Ala	Glu	Val	Asp	Met	Ile	Lys	Leu	Gln	Leu	Lys	Leu	Gln	Gly	
		1075				1080						1085				
agc	gtg	agt	gtt	cag	gtc	aat	gct	ggc	cca	cta	gca	tat	gcg	cga	gct	3312
Ser	Val	Ser	Val	Gln	Val	Asn	Ala	Gly	Pro	Leu	Ala	Tyr	Ala	Arg	Ala	
	1090					1095				1100						
ttc	tta	gat	gat	aca	aac	aca	aag	cga	tat	cct	gac	aat	aaa	gtg	aag	3360
Phe	Leu	Asp	Asp	Thr	Asn	Thr	Lys	Arg	Tyr	Pro	Asp	Asn	Lys	Val	Lys	
1105				1110					1115					1120		
ctg	ctt	aag	gaa	gtt	ttc	agg	caa	ttt	gtg	gaa	gct	tgc	ggg	caa	gcc	3408
Leu	Leu	Lys	Glu	Val	Phe	Arg	Gln	Phe	Val	Glu	Ala	Cys	Gly	Gln	Ala	
			1125				1130						1135			
tta	gcg	gta	aac	gaa	cgt	ctg	att	aaa	gaa	gac	cag	ctc	gag	tat	cag	3456
Leu	Ala	Val	Asn	Glu	Arg	Leu	Ile	Lys	Glu	Asp	Gln	Leu	Glu	Tyr	Gln	
		1140					1145					1150				
gaa	gaa	atg	aaa	gcc	aac	tac	agg	gaa	atg	gcg	aag	gag	ctt	tct	gaa	3504
Glu	Glu	Met	Lys	Ala	Asn	Tyr	Arg	Glu	Met	Ala	Lys	Glu	Leu	Ser	Glu	
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atc	atg	cat	gag	cag	atc	tgc	ccc	ctg	gag	gag	aag	acg	agc	gtc	tta	3552
Ile	Met	His	Glu	Gln	Ile	Cys	Pro	Leu	Glu	Glu	Lys	Thr	Ser	Val	Leu	
	1170				1175						1180					
ccg	aat	tcc	ctt	cac	atc	ttc	aac	gcc	atc	agt	ggg	act	cca	aca	agc	3600
Pro	Asn	Ser	Leu	His	Ile	Phe	Asn	Ala	Ile	Ser	Gly	Thr	Pro	Thr	Ser	
1185				1190					1195					1200		
aca	atg	gtt	cac	ggg	atg	acc	agc	tcg	tct	tcg	gtc	gtg	tga			3642
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1205

1210

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 35 40 45
 Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala
 50 55 60
 Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr
 65 70 75 80
 Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser
 85 90 95
 Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys
 100 105 110
 Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg
 115 120 125
 Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val
 130 135 140
 Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu
 145 150 155 160
 Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys
 165 170 175
 Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr
 180 185 190
 Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys
 195 200 205
 Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu
 210 215 220
 Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp
 225 230 235 240
 Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe
 245 250 255
 Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe
 260 265 270
 Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile
 275 280 285
 Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg
 290 295 300
 Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val
 305 310 315 320
 Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly
 325 330 335
 Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu
 340 345 350
 Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp
 355 360 365
 Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr
 370 375 380
 Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile
 385 390 395 400

Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser
 405 410 415
 Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val
 420 425 430
 Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met
 435 440 445
 Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr
 450 455 460
 Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile
 465 470 475 480
 Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile
 485 490 495
 Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser
 500 505 510
 Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg
 515 520 525
 Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser
 530 535 540
 Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala
 545 550 555 560
 Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu
 565 570 575
 Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn
 580 585 590
 Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys
 595 600 605
 His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser
 610 615 620
 Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met
 625 630 635 640
 Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu
 645 650 655
 Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg
 660 665 670
 Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu
 675 680 685
 Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile
 690 695 700
 Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala
 705 710 715 720
 Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys
 725 730 735
 Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met
 740 745 750
 Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser
 755 760 765
 Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu
 770 775 780
 Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala
 785 790 795 800
 Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr
 805 810 815
 Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr
 820 825 830
 Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Lys Ala
 835 840 845
 Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile Ile Pro Ile
 850 855 860
 Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu Tyr Asp Thr
 865 870 875 880
 Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His Ser Gly Arg

• Q26
 unX

885 890 895
 Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe Gly Gln Gly Phe
 900 905 910
 Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu
 915 920 925
 Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp
 930 935 940
 Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val
 945 950 955 960
 Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His
 965 970 975
 Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu
 980 985 990
 Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe
 995 1000 1005
 Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg
 1010 1015 1020
 Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1025 1030 1035 1040
 Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 1045 1050 1055
 Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys
 1060 1065 1070
 Ser Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly
 1075 1080 1085
 Ser Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala
 1090 1095 1100
 Phe Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys
 1105 1110 1115 1120
 Leu Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala
 1125 1130 1135
 Leu Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln
 1140 1145 1150
 Glu Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu
 1155 1160 1165
 Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu
 1170 1175 1180
 Pro Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser
 1185 1190 1195 1200
 Thr Met Val His Gly Met Thr Ser Ser Ser Ser Val Val
 1205 1210

<210> 11
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Insertion of
 69 nucleotides at position 2927 in human CLASP-2A
 found in human CLASP-2D

<400> 11
 aagcagtcca gtgggagccg ccccttctcc cccacagcca tagcgcctgc ctgaggagga 60
 gccggggag 69

<210> 12
 <211> 22

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acids
encoded by insertion of 69 nucleotides at position
2927 of human CLASP-2A found in human CLASP-2D.

<400> 12

Ala Val Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys
1 5 10 15

Leu Arg Arg Ser Arg Gly
20

<210> 13

<211> 165

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Insertion at
position 3153, entire sequence insertion in human
CLASP-2D, portion of insertion in human CLASP-2B,
2C and 2E

<400> 13

tgagaggctg gccatctgt atgacacgct gcaccgggcc tacagcaaag tgaccgaggt 60
catgcactcg ggccgcaggc ttctggggac ctacttccgg gtagccttct tcgggcaggc 120
agcgcaatac cagtttacag acagtgaac agatgtggag ggatt 165

926
cont.
<210> 14

<211> 54

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acids
encoded by entire insertion at position 3153 of
human CLASP-2A found in human CLASP-2D

<400> 14

Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
1 5 10 15

Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
20 25 30

Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
35 40 45

Glu Thr Asp Val Glu Gly
50

<210> 15

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acids
encoded by insertion at position 3153 of human
CLASP-2A found in human CLASP-2B, 2C and 2E

<400> 15

Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
1 5 10 15

Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
20 25 30

Arg Val Ala Phe Phe Gly Gln Gly
35 40

<210> 16

<211> 3614

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3) .. (2864)

<220>

<223> Human cadherin-like asymmetry protein 2A-80
(CLASP-2A-80)

<400> 16

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Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe
1 5 10 15

ttg gtg gga ctg tta ctg agg gag gtg ggg aca gcc ctc cag gag ttc 95
Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe
20 25 30

cgg gag gtc cgt ctg atc gcc atc agt gtg ctc aag aac ctg ctg ata 143
Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile
35 40 45

aag cat tct ttt gat gac aga tat gct tca agg agc cat cag gca agg 191
Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg
50 55 60

ata gcc acc ctc tac ctg cct ctg ttt ggt ctg ctg att gaa aac gtc 239
Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val
65 70 75

cag cgg atc aat gtg agg gat gtg tca ccc ttc cct gtg aac gcg ggc 287
Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly
80 85 90 95

atg acc gtg aag gat gaa tcc ctg gct cta cca gct gtg aat ccg ctg 335
Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu
100 105 110

gtg acg ccg cag aag gga agc acc ctg gac aac agc ctg cac aag gac 383
Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp

115	120	125	
ctg ctg ggc gcc atc tcc ggc att gct tct cca tat aca acc tca act Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr 130 135 140			431
cca aac atc aac agt gtg aga aat gct gat tcg aga gga tct ctc ata Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile 145 150 155			479
agc aca gat tcg ggt aac agc ctt cca gaa agg aat agt gag aag agc Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser 160 165 170 175			527
aat tcc ctg gat aag cac caa caa agt agc aca ttg gga aat tcc gtg Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val 180 185 190			575
gtt cgc tgt gat aaa ctt gac cag tct gag att aag agc cta ctg atg Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met 195 200 205			623
tgt ttc ctc tac atc tta aag agc atg tct gat gat gct ttg ttt aca Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr 210 215 220			671
tat tgg aac aag gct tca aca tct gaa ctt atg gat ttt ttt aca ata Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile 225 230 235			719
tct gaa gtc tgc ctg cac cag ttc cag tac atg ggg aag cga tac ata Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile 240 245 250 255			767
gcc agg aac cag gag ggg ttg gga ccc ata gtt cat gat cga aag tct Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser 260 265 270			815
cag aca ttg cct gtt tcc cgt aac aga aca gga atg atg cat gcc aga Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg 275 280 285			863
ttg cag cag ctg ggc agc ctg gat aac tct ctc act ttt aac cac agc Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser 290 295 300			911
tat ggc cac tcg gac gca gat gtt ctg cac cag tca tta ctt gaa gcc Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala 305 310 315			959
aac att gct act gag gtt tgc ctg aca gct ctg gac acg ctt tct cta Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu 320 325 330 335			1007
ttt aca ttg gcg ttt aag aac cag ctc ctg gcc gac cat gga cat aat Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn 340 345 350			1055
cct ctc atg aaa aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys 355 360 365			1103

Q26
cont.

cat cag tct gaa acg gct tta aaa aat gtc ttc act gcc tta agg tcc	1151
His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser	
370 375 380	
tta att tat aag ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg	1199
Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met	
385 390 395	
tgt gcg gct ctg tgt tac gag att ctc aag tgc tgt aac tcc aag ctg	1247
Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu	
400 405 410 415	
agc tcc atc agg acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg	1295
Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg	
420 425 430	
aac aac ttt gat tac act gga aag aag tcc ttt gtc cgg aca cat ttg	1343
Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu	
435 440 445	
caa gtc atc ata tct gtc agc cag ctg ata gca gac gtt gtt ggc att	1391
Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile	
450 455 460	
ggg gaa acc aga ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc	1439
Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala	
465 470 475	
aac agt gac cgg ctt att aag cac acc agc ttc tcc tct gat gtg aag	1487
Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys	
480 485 490 495	
gac tta acc aaa agg ata cgc acg gtg cta atg gcc acc gcc cag atg	1535
Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met	
500 505 510	
aag gag cat gag aac gac cca gag atg ctg gtg gac ctc cag tac agc	1583
Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser	
515 520 525	
ctg gcc aaa tcc tat gcc agc acg ccc gag ctc agg aag acg tgg ctc	1631
Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu	
530 535 540	
gac agc atg gcc agg atc cat gtc aaa aat ggc gat ctc tca gag gca	1679
Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala	
545 550 555	
gca atg tgc tat gtc cac gta aca gcc cta gtg gca gaa tat ctc aca	1727
Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr	
560 565 570 575	
cgg aaa ggc gtg ttt aga caa gga tgc acc gcc ttc agg gtc att acc	1775
Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr	
580 585 590	
cca aac atc gac gag gag gcc tcc atg atg gaa gac gtg ggg atg cag	1823
Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln	
595 600 605	

a26
ent.

gat	gtc	cat	ttc	aac	gag	gat	gtg	ctg	atg	gag	ctc	ctt	gag	cag	tgc	1871
Asp	Val	His	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln	Cys	
		610					615					620				
gca	gat	gga	ctc	tgg	aaa	gcc	gag	cgc	tac	gag	ctc	atc	gcc	gac	atc	1919
Ala	Asp	Gly	Leu	Trp	Lys	Ala	Glu	Arg	Tyr	Glu	Leu	Ile	Ala	Asp	Ile	
	625					630					635					
tac	aaa	ctt	atc	atc	ccc	att	tat	gag	aag	cgg	agg	gat	ttc	ttt	gaa	1967
Tyr	Lys	Leu	Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe	Phe	Glu	
640					645					650					655	
gat	gaa	gat	gga	aag	gag	tat	att	tac	aag	gaa	ccc	aaa	ctc	aca	ccg	2015
Asp	Glu	Asp	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	
				660					665					670		
ctg	tcg	gaa	att	tct	cag	aga	ctc	ctt	aaa	ctg	tac	tcg	gat	aaa	ttt	2063
Leu	Ser	Glu	Ile	Ser	Gln	Arg	Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	
			675					680					685			
ggt	tct	gaa	aat	gtc	aaa	atg	ata	cag	gat	tct	ggc	aag	gtc	aac	cct	2111
Gly	Ser	Glu	Asn	Val	Lys	Met	Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	
		690					695					700				
aag	gat	ctg	gat	tct	aag	tat	gca	tac	atc	cag	gtg	act	cac	gtc	atc	2159
Lys	Asp	Leu	Asp	Ser	Lys	Tyr	Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Ile	
	705					710					715					
ccc	ttc	ttt	gac	gaa	aaa	gag	ttg	caa	gaa	agg	aaa	aca	gag	ttt	gag	2207
Pro	Phe	Phe	Asp	Glu	Lys	Glu	Leu	Gln	Glu	Arg	Lys	Thr	Glu	Phe	Glu	
720					725					730					735	
aga	tcc	cac	aac	atc	cgc	cgc	ttc	atg	ttt	gag	atg	cca	ttt	acg	cag	2255
Arg	Ser	His	Asn	Ile	Arg	Arg	Phe	Met	Phe	Glu	Met	Pro	Phe	Thr	Gln	
				740					745					750		
acc	ggg	aag	agg	cag	ggc	ggg	gtg	gaa	gag	cag	tgc	aaa	cgg	cgc	acc	2303
Thr	Gly	Lys	Arg	Gln	Gly	Gly	Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	
			755					760					765			
atc	ctg	aca	gcc	ata	cac	tgc	ttc	cct	tat	gtg	aag	aag	cgc	atc	cct	2351
Ile	Leu	Thr	Ala	Ile	His	Cys	Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	
		770					775					780				
gtc	atg	tac	cag	cac	cac	act	gac	ctg	aac	ccc	atc	gag	gtg	gcc	att	2399
Val	Met	Tyr	Gln	His	His	Thr	Asp	Leu	Asn	Pro	Ile	Glu	Val	Ala	Ile	
	785					790					795					
gac	gag	atg	agt	aag	aag	gtg	gcg	gag	ctc	cgg	cag	ctg	tgc	tcc	tcg	2447
Asp	Glu	Met	Ser	Lys	Lys	Val	Ala	Glu	Leu	Arg	Gln	Leu	Cys	Ser	Ser	
800					805					810					815	
gcc	gag	gtg	gac	atg	atc	aaa	ctg	cag	ctc	aaa	ctc	cag	ggc	agc	gtg	2495
Ala	Glu	Val	Asp	Met	Ile	Lys	Leu	Gln	Leu	Lys	Leu	Gln	Gly	Ser	Val	
				820					825					830		
agt	gtt	cag	gtc	aat	gct	ggc	cca	cta	gca	tat	gcg	cga	gct	ttc	tta	2543
Ser	Val	Gln	Val	Asn	Ala	Gly	Pro	Leu	Ala	Tyr	Ala	Arg	Ala	Phe	Leu	
			835					840					845			
gat	gat	aca	aac	aca	aag	cga	tat	cct	gac	aat	aaa	gtg	aag	ctg	ctt	2591

a26
cont.

Asp	Asp	Thr	Asn	Thr	Lys	Arg	Tyr	Pro	Asp	Asn	Lys	Val	Lys	Leu	Leu	
		850					855					860				
aag	gaa	gtt	ttc	agg	caa	ttt	gtg	gaa	gct	tgc	ggg	caa	gcc	tta	gcg	2639
Lys	Glu	Val	Phe	Arg	Gln	Phe	Val	Glu	Ala	Cys	Gly	Gln	Ala	Leu	Ala	
	865					870					875					
gta	aac	gaa	cgt	ctg	att	aaa	gaa	gac	cag	ctc	gag	tat	cag	gaa	gaa	2687
Val	Asn	Glu	Arg	Leu	Ile	Lys	Glu	Asp	Gln	Leu	Glu	Tyr	Gln	Glu	Glu	
	880				885					890					895	
atg	aaa	gcc	aac	tac	agg	gaa	atg	gag	aag	gag	ctt	tct	gaa	atc	atg	2735
Met	Lys	Ala	Asn	Tyr	Arg	Glu	Met	Ala	Lys	Glu	Leu	Ser	Glu	Ile	Met	
				900					905					910		
cat	gag	cag	atc	tgc	ccc	ctg	gag	gag	aag	acg	agc	gtc	tta	ccg	aat	2783
His	Glu	Gln	Ile	Cys	Pro	Leu	Glu	Glu	Lys	Thr	Ser	Val	Leu	Pro	Asn	
			915				920						925			
tcc	ctt	cac	atc	ttc	aac	gcc	atc	agt	ggg	act	cca	aca	agc	aca	atg	2831
Ser	Leu	His	Ile	Phe	Asn	Ala	Ile	Ser	Gly	Thr	Pro	Thr	Ser	Thr	Met	
		930				935						940				
gtt	cac	ggg	atg	acc	agc	tcg	tct	tcg	gtc	gtg	tgattacatc	tcattggcccg				2884
Val	His	Gly	Met	Thr	Ser	Ser	Ser	Ser	Val	Val						
	945					950										
tgtgtgggga	cttgctttgt	catttgcaaa	ctcaggatgc	tttccaaagc	caatcactgg											2944
ggagaccgag	cacagggagg	accaagggga	aggggagaga	aaggaaataa	agaacaacgt											3004
tatttcttaa	cagactttct	ataggagttg	taagaagggtg	cacatatttt	tttaaattctc											3064
actggcaata	ttcaaagttt	tcattgtgtc	ttaacaaagg	tgtggtagac	actcttgagc											3124
tggacttaga	ttttattctt	ccttgcagag	tagtgttaga	atagatggcc	tacagaaaaa											3184
aaaggttctg	ggatctacat	ggcagggagg	gctgcactga	cattgatgcc	tgggggacct											3244
tttgccctga	ctcgtgccgg	aatctgatc	gtaatcaggg	tacagaactt	actagttttg											3304
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agaatagtga	gctaactgag	ctagacactc	aattaatccg	ctactggctt	caagtcagaa											3424
ctttgtcatt	aatcatcgac	tcggggacgg	tcatatatgt	attacatttc	tacattttta											3484
atactcacat	gggcttatgc	attaagttta	attgtgataa	atttgtgctg	gtccagtata											3544
tgcaatacac	tttaatgggt	tattcttgct	ataaaaaatgt	gcaatatgga	gatgtataca											3604
agtctttact																3614

<210> 17
 <211> 954
 <212> PRT
 <213> Homo sapiens
 <223> Human cadherin-like asymmetry protein 2A-80
 (CLASP-2A-80)

<400> 17

Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu
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Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg
20 25 30
Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys
35 40 45
His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile
50 55 60
Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln
65 70 75 80
Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met
85 90 95
Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val
100 105 110
Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu
115 120 125
Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro
130 135 140
Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser
145 150 155 160
Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn
165 170 175
Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val
180 185 190
Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys
195 200 205
Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr
210 215 220
Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser
225 230 235 240
Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala
245 250 255
Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln
260 265 270
Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu
275 280 285
Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr
290 295 300
Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn
305 310 315 320

026
cont.

Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe
 325 330 335
 Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro
 340 345 350
 Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His
 355 360 365
 Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu
 370 375 380
 Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys
 385 390 395 400
 Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser
 405 410 415
 Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn
 420 425 430
 Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln
 435 440 445
 Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly
 450 455 460
 Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn
 465 470 475 480
 Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp
 485 490 495
 Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys
 500 505 510
 Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu
 515 520 525
 Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp
 530 535 540
 Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala
 545 550 555 560
 Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg
 565 570 575
 Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro
 580 585 590
 Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp
 595 600 605
 Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala
 610 615 620
 Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr
 625 630 635 640
 Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp

a26
 cont.

645					650					655					
Glu	Asp	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu
		660						665					670		
Ser	Glu	Ile	Ser	Gln	Arg	Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly
		675					680					685			
Ser	Glu	Asn	Val	Lys	Met	Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys
		690				695					700				
Asp	Leu	Asp	Ser	Lys	Tyr	Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Ile	Pro
705					710					715					720
Phe	Phe	Asp	Glu	Lys	Glu	Leu	Gln	Glu	Arg	Lys	Thr	Glu	Phe	Glu	Arg
				725					730					735	
Ser	His	Asn	Ile	Arg	Arg	Phe	Met	Phe	Glu	Met	Pro	Phe	Thr	Gln	Thr
			740					745					750		
Gly	Lys	Arg	Gln	Gly	Gly	Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile
		755					760					765			
Leu	Thr	Ala	Ile	His	Cys	Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val
		770				775					780				
Met	Tyr	Gln	His	His	Thr	Asp	Leu	Asn	Pro	Ile	Glu	Val	Ala	Ile	Asp
785					790					795					800
Glu	Met	Ser	Lys	Lys	Val	Ala	Glu	Leu	Arg	Gln	Leu	Cys	Ser	Ser	Ala
				805					810					815	
Glu	Val	Asp	Met	Ile	Lys	Leu	Gln	Leu	Lys	Leu	Gln	Gly	Ser	Val	Ser
			820					825					830		
Val	Gln	Val	Asn	Ala	Gly	Pro	Leu	Ala	Tyr	Ala	Arg	Ala	Phe	Leu	Asp
			835				840					845			
Asp	Thr	Asn	Thr	Lys	Arg	Tyr	Pro	Asp	Asn	Lys	Val	Lys	Leu	Leu	Lys
						855					860				
Glu	Val	Phe	Arg	Gln	Phe	Val	Glu	Ala	Cys	Gly	Gln	Ala	Leu	Ala	Val
865					870					875					880
Asn	Glu	Arg	Leu	Ile	Lys	Glu	Asp	Gln	Leu	Glu	Tyr	Gln	Glu	Glu	Met
				885					890					895	
Lys	Ala	Asn	Tyr	Arg	Glu	Met	Ala	Lys	Glu	Leu	Ser	Glu	Ile	Met	His
			900					905					910		
Glu	Gln	Ile	Cys	Pro	Leu	Glu	Glu	Lys	Thr	Ser	Val	Leu	Pro	Asn	Ser
			915				920					925			
Leu	His	Ile	Phe	Asn	Ala	Ile	Ser	Gly	Thr	Pro	Thr	Ser	Thr	Met	Val
						935					940				
His	Gly	Met	Thr	Ser	Ser	Ser	Ser	Val	Val						
945					950										

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 <213> Homo sapiens

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 (CLASP-2F)

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 cca gaa agg aat agt gag aag agc aat tcc ctg gat aag cac caa caa 96
 Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys His Gln Gln
 20 25 30
 agt agc aca ttg gga aat tcc gtg gtt cgc tgt gat aaa ctt gac cag 144
 Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp Lys Leu Asp Gln
 35 40 45
 tct gag att aag agc cta ctg atg tgt ttc ctc tac atc tta aag agc 192
 Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser
 50 55 60
 atg tct gat gat gct ttg ttt aca tat tgg aac aag gct tca aca tct 240
 Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser
 65 70 75 80
 gaa ctt atg gat ttt ttt aca ata tct gaa gtc tgc ctg cac cag ttc 288
 Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val Cys Leu His Gln Phe
 85 90 95
 cag tac atg ggg aag cga tac ata gcc agt gtg aga aag ata tca agt 336
 Gln Tyr Met Gly Lys Arg Tyr Ile Ala Ser Val Arg Lys Ile Ser Ser
 100 105 110
 gtg ctt gga att tct gta gac aat ggc tat ggc cac tcg gac gca gat 384
 Val Leu Gly Ile Ser Val Asp Asn Gly Tyr Gly His Ser Asp Ala Asp
 115 120 125
 gtt ctg cac cag tca tta ctt gaa gcc aac att gct act gag gtt tgc 432
 Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu Val Cys
 130 135 140
 ctg aca gct ctg gac acg ctt tct cta ttt aca ttg gcg ttt aag aac 480
 Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe Lys Asn
 145 150 155 160
 cag ctc ctg gcc gac cat gga cat aat cct ctc atg aaa aaa aaa a 526
 Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys Lys
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<210> 19
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 <213> Homo sapiens
 <223> Human cadherin-like asymmetry protein 2F
 (CLASP-2F)

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 Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys His Gln Gln
 20 25 30
 Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp Lys Leu Asp Gln
 35 40 45
 Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser
 50 55 60
 Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser
 65 70 75 80
 Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val Cys Leu His Gln Phe
 85 90 95
 Gln Tyr Met Gly Lys Arg Tyr Ile Ala Ser Val Arg Lys Ile Ser Ser
 100 105 110
 Val Leu Gly Ile Ser Val Asp Asn Gly Tyr Gly His Ser Asp Ala Asp
 115 120 125
 Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu Val Cys
 130 135 140
 Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe Lys Asn
 145 150 155 160
 Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys Lys
 165 170 175

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 <211> 738
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> Rat TRG protein

<400> 20

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 1 5 10 15
 Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn
 20 25 30
 Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe
 35 40 45
 Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu
 50 55 60

Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser	Ile	Arg	Thr	Glu	Ala	Ser	Gln
65					70					75					80
Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn	Phe	Asp	Tyr	Thr	Gly	Lys	Lys
				85					90					95	
Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val	Ile	Ile	Ser	Leu	Ser	Gln	Leu
			100					105					110		
Ile	Ala	Asp	Val	Val	Gly	Ile	Gly	Gly	Thr	Arg	Phe	Gln	Gln	Ser	Leu
		115					120					125			
Ser	Ile	Ile	Asn	Asn	Cys	Ala	Asn	Ser	Asp	Arg	Leu	Ile	Lys	His	Thr
	130					135					140				
Ser	Phe	Ser	Ser	Asp	Val	Lys	Asp	Leu	Thr	Lys	Arg	Ile	Arg	Thr	Val
145					150					155					160
Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Asn	Asp	Pro	Glu	Met
				165					170					175	
Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	Ser	Tyr	Ala	Ser	Thr	Pro
			180					185					190		
Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	Ala	Arg	Ile	His	Val	Lys
		195					200					205			
Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Val	His	Val	Thr	Ala
	210					215					220				
Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Glu	Ala	Asp	Leu	Ala	Leu	Gln
225					230					235					240
Arg	Glu	Pro	Pro	Val	Phe	Pro	Tyr	Ser	His	Thr	Ser	Cys	Gln	Arg	Lys
				245					250					255	
Ser	Arg	Gly	Gly	Met	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile
			260					265					270		
Thr	Pro	Asn	Ile	Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Met
		275					280					285			
Gln	Asp	Val	His	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln
	290					295					300				
Cys	Ala	Asp	Gly	Leu	Trp	Lys	Ala	Glu	Arg	Leu	Arg	Ala	Gly	Leu	Leu
305					310					315					320
Thr	Ser	Ile	Asn	Ser	Ser	Ser	Pro	Ser	Met	Lys	Ser	Gly	Gly	Thr	Leu
			325						330					335	
Glu	Thr	Thr	His	Leu	Tyr	Asp	Thr	Leu	His	Arg	Pro	Tyr	Ser	Lys	Val
			340					345					350		
Thr	Glu	Val	Ile	Thr	Arg	Ala	Ala	Gly	Ser	Trp	Asp	Leu	Leu	Pro	Gly
		355					360					365			
Gly	Leu	Phe	Gly	Gln	Gly	Phe	Phe	Glu	Asp	Glu	Asp	Gly	Lys	Glu	Tyr
	370					375					380				

a26
cont.

Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	Ile	Ser	Gln	Arg	385	390	395	400
Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	Asn	Val	Lys	Met		405	410	415
Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	Asp	Ser	Lys	Phe		420	425	430
Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Thr	Pro	Phe	Phe	Asp	Glu	Lys	Glu		435	440	445
Leu	Gln	Glu	Arg	Lys	Thr	Glu	Phe	Glu	Arg	Cys	His	Asn	Ile	Arg	Arg		450	455	460
Phe	Met	Phe	Glu	Met	Pro	Phe	Thr	Gln	Thr	Gly	Lys	Arg	Gln	Gly	Gly	465	470	475	480
Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	Ala	Ile	His	Cys		485	490	495
Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	Tyr	Gln	His	His	Thr		500	505	510
Asp	Leu	Asn	Pro	Ile	Glu	Val	Ala	Ile	Asp	Glu	Met	Ser	Lys	Lys	Val		515	520	525
Ala	Glu	Leu	His	Gln	Leu	Cys	Ser	Ser	Ala	Glu	Val	Asp	Met	Ile	Lys		530	535	540
Leu	Gln	Leu	Lys	Leu	Gln	Gly	Ser	Val	Ser	Val	Gln	Val	Asn	Ala	Gly	545	550	555	560
Pro	Leu	Ala	Tyr	Ala	Arg	Ala	Phe	Leu	Asp	Asp	Thr	Asn	Thr	Lys	Arg		565	570	575
Tyr	Pro	Asp	Asn	Lys	Val	Lys	Leu	Leu	Lys	Glu	Val	Phe	Arg	Gln	Phe		580	585	590
Val	Glu	Ala	Cys	Gly	Gln	Ala	Leu	Ala	Val	Asn	Glu	Arg	Leu	Ile	Lys		595	600	605
Glu	Asp	Gln	Leu	Glu	Tyr	Gln	Glu	Glu	Met	Lys	Ala	Asn	Tyr	Arg	Glu		610	615	620
Ile	Arg	Lys	Glu	Leu	Ser	Asp	Ile	Ile	Val	Pro	Arg	Ile	Cys	Pro	Gly	625	630	635	640
Glu	Asp	Lys	Arg	Ala	Thr	Lys	Phe	Pro	Ala	His	Leu	Gln	Arg	His	Gln		645	650	655
Arg	Asp	Thr	Asn	Lys	His	Ser	Gly	Ser	Arg	Val	Asp	Gln	Phe	Ile	Leu		660	665	670
Ser	Cys	Val	Thr	Leu	Pro	His	Glu	Pro	His	Val	Gly	Thr	Cys	Phe	Val		675	680	685
Met	Cys	Lys	Leu	Arg	Thr	Thr	Phe	Arg	Ala	Asn	His	Trp	Phe	Cys	Gln		690	695	700
Ala	Gln	Glu	Glu	Ala	Met	Gly	Asn	Gly	Arg	Glu	Lys	Glu	Pro	Trp	Thr				

Q76
mk-

225					230					235					240
Asn	Leu	Glu	Tyr	Ser	Leu	Ser	Asp	Glu	Tyr	Cys	Lys	His	His	Phe	Leu
				245					250					255	
Val	Gly	Leu	Leu	Leu	Arg	Glu	Thr	Ser	Ile	Ala	Leu	Gln	Asp	Asn	Tyr
		260						265					270		
Glu	Ile	Arg	Tyr	Thr	Ala	Ile	Ser	Val	Ile	Lys	Asn	Leu	Leu	Ile	Lys
		275					280					285			
His	Ala	Phe	Asp	Thr	Arg	Tyr	Gln	His	Lys	Asn	Gln	Gln	Ala	Lys	Ile
	290					295					300				
Ala	Gln	Leu	Tyr	Leu	Pro	Phe	Val	Gly	Leu	Leu	Leu	Glu	Asn	Ile	Gln
305					310					315					320
Arg	Leu	Ala	Gly	Arg	Asp	Thr	Leu	Tyr	Ser	Cys	Ala	Ala	Met	Pro	Asn
				325					330					335	
Ser	Ala	Ser	Arg	Asp	Glu	Phe	Pro	Cys	Gly	Phe	Thr	Ser	Pro	Ala	Asn
			340					345					350		
Arg	Gly	Ser	Leu	Ser	Thr	Asp	Lys	Asp	Thr	Ala	Tyr	Gly	Ser	Phe	Gln
		355					360					365			
Asn	Gly	His	Gly	Ile	Lys	Arg	Glu	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Pro
	370					375					380				
Glu	Gly	Ala	Thr	Gly	Phe	Pro	Asp	Gln	Gly	Asn	Thr	Gly	Glu	Asn	Thr
385					390					395					400
Arg	Gln	Ser	Ser	Thr	Arg	Ser	Ser	Val	Ser	Gln	Tyr	Asn	Arg	Leu	Asp
				405					410					415	
Gln	Tyr	Glu	Ile	Arg	Ser	Leu	Leu	Met	Cys	Tyr	Leu	Tyr	Ile	Val	Lys
			420					425					430		
Met	Ile	Ser	Glu	Asp	Thr	Leu	Leu	Thr	Tyr	Trp	Asn	Lys	Val	Ser	Pro
		435					440					445			
Gln	Glu	Leu	Ile	Asn	Ile	Leu	Ile	Leu	Leu	Glu	Val	Cys	Leu	Phe	His
	450					455					460				
Phe	Arg	Tyr	Met	Gly	Lys	Arg	Asn	Ile	Ala	Arg	Val	His	Asp	Ala	Trp
465					470					475					480
Leu	Ser	Lys	His	Phe	Gly	Ile	Asp	Arg	Lys	Ser	Gln	Thr	Met	Pro	Ala
				485				490						495	
Leu	Arg	Asn	Arg	Ser	Gly	Val	Met	Gln	Ala	Arg	Leu	Gln	His	Leu	Ser
		500						505					510		
Ser	Leu	Glu	Ser	Ser	Phe	Thr	Leu	Asn	His	Ser	Ser	Thr	Thr	Thr	Glu
		515					520					525			
Ala	Asp	Ile	Phe	His	Gln	Ala	Leu	Leu	Glu	Gly	Asn	Thr	Ala	Thr	Glu
	530					535					540				
Val	Ser	Leu	Thr	Val	Leu	Asp	Thr	Ile	Ser	Phe	Phe	Thr	Gln	Cys	Phe
545					550					555					560

926
cont.

Lys Thr His Phe Leu Asn Asn Asp Gly His Asn Pro Leu Met Lys Lys
 565 570 575
 Val Phe Asp Ile His Leu Ala Phe Leu Lys Asn Gly Gln Ser Glu Val
 580 585 590
 Ser Leu Lys His Val Phe Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe
 595 600 605
 Pro Ser Ala Phe Phe Lys Gly Arg Val Asn Met Cys Ala Ala Phe Cys
 610 615 620
 Tyr Glu Val Leu Lys Cys Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn
 625 630 635 640
 Glu Ala Ser Ala Leu Leu Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr
 645 650 655
 Thr Lys Arg Lys Thr Phe Leu Arg Thr His Leu Gln Ile Ile Ile Ala
 660 665 670
 Val Ser Gln Leu Ile Ala Asp Val Ala Leu Ser Gly Gly Ser Arg Phe
 675 680 685
 Gln Glu Ser Leu Phe Ile Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro
 690 695 700
 Met Leu Ala Arg Ala Phe Pro Ala Glu Val Lys Asp Leu Thr Lys Arg
 705 710 715 720
 Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Lys
 725 730 735
 Asp Pro Glu Met Leu Ile Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
 740 745 750
 Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Lys
 755 760 765
 Ile His Val Lys Asn Gly Asp Phe Ser Glu Ala Ala Met Cys Tyr Val
 770 775 780
 His Val Ala Ala Leu Val Ala Glu Phe Leu His Arg Lys Lys Leu Phe
 785 790 795 800
 Pro Asn Gly Cys Ser Ala Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu
 805 810 815
 Glu Gly Ala Met Lys Glu Asp Ala Gly Met Met Asp Val His Tyr Ser
 820 825 830
 Glu Glu Val Leu Leu Glu Leu Leu Glu Gln Cys Val Asn Gly Leu Trp
 835 840 845
 Lys Ala Glu Arg Tyr Glu Ile Ile Ser Glu Ile Ser Lys Leu Ile Gly
 850 855 860
 Pro Ile Tyr Glu Asn Arg Arg Glu Phe Glu Asn Leu Thr Gln Val Tyr
 865 870 875 880

a26
 cont.

Arg Thr Leu His Gly Ala Tyr Thr Lys Ile Leu Glu Val Met His Thr
 885 890 895
 Lys Lys Arg Leu Leu Gly Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln
 900 905 910
 Ser Phe Phe Glu Glu Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
 915 920 925
 Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr
 930 935 940
 Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser Asp
 945 950 955 960
 Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln Val
 965 970 975
 Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys
 980 985 990
 Thr Glu Phe Glu Arg Asn His Asn Ile Ser Arg Phe Val Phe Glu Ala
 995 1000 1005
 Pro Tyr Thr Leu Ser Gly Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys
 1010 1015 1020
 Lys Arg Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys
 1025 1030 1035 1040
 Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile
 1045 1050 1055
 Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys
 1060 1065 1070
 Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu
 1075 1080 1085
 Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala
 1090 1095 1100
 Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys
 1105 1110 1115 1120
 Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser
 1125 1130 1135
 Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu
 1140 1145 1150
 Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu
 1155 1160 1165
 Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser
 1170 1175 1180
 Pro Trp Met Ser Asn Thr Leu His Val Phe Cys Ala Ile Ser Gly Thr
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 Ser Ser Asp Arg Gly Tyr Gly Ser Pro Arg Tyr Ala Glu Val

076
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1205

1210

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 <212> PRT
 <213> Homo sapiens

<220>
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 Asp Ile Val Ala Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln
 35 40 45
 Ser Tyr Ile Lys Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro
 50 55 60
 Val His Glu Asp Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn
 65 70 75 80
 Asp Ser Pro Thr Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe
 85 90 95
 Ala Ile Ile Leu Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys
 100 105 110
 Ile Gln Leu Pro Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu
 115 120 125
 Leu Asp Asn Leu Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr
 130 135 140
 Lys Asp Ala Leu Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg
 145 150 155 160
 Phe Leu Lys Arg Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys
 165 170 175
 Met Val Asn Asn Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr
 180 185 190
 Leu Cys Gln Tyr Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu
 195 200 205
 His Phe Ile Pro Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp
 210 215 220
 Pro Leu Thr Pro Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met
 225 230 235 240
 Pro Glu Tyr Ser Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile
 245 250 255
 Gly Ile Leu Leu Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp

all
 cont.

260						265						270					
Val	Arg	His	Leu	Ala	Leu	Ala	Val	Leu	Lys	Asn	Leu	Met	Ala	Lys	His		
		275					280					285					
Ser	Phe	Asp	Asp	Arg	Tyr	Arg	Glu	Pro	Arg	Lys	Gln	Ala	Gln	Ile	Ala		
	290					295					300						
Ser	Leu	Tyr	Met	Pro	Leu	Tyr	Gly	Met	Leu	Leu	Asp	Asn	Met	Pro	Arg		
305					310					315					320		
Ile	Tyr	Leu	Lys	Asp	Leu	Tyr	Pro	Phe	Thr	Val	Asn	Thr	Ser	Asn	Gln		
				325					330					335			
Gly	Ser	Arg	Asp	Asp	Leu	Ser	Thr	Asn	Gly	Gly	Phe	Gln	Ser	Gln	Thr		
			340					345					350				
Ala	Ile	Lys	His	Ala	Asn	Ser	Val	Asp	Thr	Ser	Phe	Ser	Lys	Asp	Val		
		355					360					365					
Leu	Asn	Ser	Ile	Ala	Ala	Phe	Ser	Ser	Ile	Ala	Ile	Ser	Thr	Val	Asn		
	370					375					380						
His	Ala	Asp	Ser	Arg	Ala	Ser	Leu	Ala	Ser	Leu	Asp	Ser	Asn	Pro	Ser		
385					390					395				400			
Thr	Asn	Glu	Lys	Ser	Ser	Glu	Lys	Thr	Asp	Asn	Cys	Glu	Lys	Ile	Pro		
				405					410					415			
Arg	Pro	Leu	Ala	Leu	Ile	Gly	Ser	Thr	Leu	Arg	Phe	Asp	Arg	Leu	Asp		
			420					425					430				
Gln	Ala	Glu	Thr	Arg	Ser	Leu	Leu	Met	Cys	Phe	Leu	His	Ile	Met	Lys		
		435					440					445					
Thr	Ile	Ser	Tyr	Glu	Thr	Leu	Ile	Ala	Tyr	Trp	Gln	Arg	Ala	Pro	Ser		
	450					455					460						
Pro	Glu	Val	Ser	Asp	Phe	Phe	Ser	Ile	Leu	Asp	Val	Cys	Leu	Gln	Asn		
465					470					475				480			
Phe	Arg	Tyr	Leu	Gly	Lys	Arg	Asn	Ile	Ile	Arg	Lys	Ile	Ala	Ala	Ala		
				485					490				495				
Phe	Lys	Phe	Val	Gln	Ser	Thr	Gln	Asn	Asn	Gly	Thr	Leu	Lys	Gly	Ser		
			500					505					510				
Asn	Pro	Ser	Cys	Gln	Thr	Ser	Gly	Leu	Leu	Ala	Gln	Trp	Met	His	Ser		
		515					520					525					
Thr	Ser	Arg	His	Glu	Gly	His	Lys	Gln	His	Arg	Ser	Gln	Thr	Leu	Pro		
	530					535					540						
Ile	Ile	Arg	Gly	Lys	Asn	Ala	Leu	Ser	Asn	Pro	Lys	Leu	Leu	Gln	Met		
545					550					555				560			
Leu	Asp	Asn	Thr	Met	Thr	Ser	Asn	Ser	Asn	Glu	Ile	Asp	Ile	Val	His		
				565					570				575				
His	Val	Asp	Thr	Glu	Ala	Asn	Ile	Ala	Thr	Glu	Gly	Cys	Leu	Thr	Ile		
			580				585						590				

arb
cont.

Leu	Asp	Leu	Val	Ser	Leu	Phe	Thr	Gln	Thr	His	Gln	Arg	Gln	Leu	Gln
	595						600					605			
Gln	Cys	Asp	Cys	Gln	Asn	Ser	Leu	Met	Lys	Arg	Gly	Phe	Asp	Thr	Tyr
	610					615					620				
Met	Leu	Phe	Phe	Gln	Val	Asn	Gln	Ser	Ala	Thr	Ala	Leu	Lys	His	Val
625					630					635					640
Phe	Ala	Ser	Leu	Arg	Leu	Phe	Val	Cys	Lys	Phe	Pro	Ser	Ala	Phe	Phe
				645					650					655	
Gln	Gly	Pro	Ala	Asp	Leu	Cys	Gly	Ser	Phe	Cys	Tyr	Glu	Val	Leu	Lys
			660					665					670		
Cys	Cys	Asn	His	Arg	Ser	Arg	Ser	Thr	Gln	Thr	Glu	Ala	Ser	Ala	Leu
		675					680					685			
Leu	Tyr	Leu	Phe	Met	Arg	Lys	Asn	Phe	Glu	Phe	Asn	Lys	Gln	Lys	Ser
	690					695					700				
Ile	Val	Arg	Ser	His	Leu	Gln	Leu	Ile	Lys	Ala	Val	Ser	Gln	Leu	Ile
705					710					715					720
Ala	Asp	Ala	Gly	Ile	Gly	Gly	Ser	Arg	Phe	Gln	His	Ser	Leu	Ala	Ile
				725					730					735	
Thr	Asn	Asn	Phe	Ala	Asn	Gly	Asp	Lys	Gln	Met	Lys	Asn	Ser	Asn	Phe
			740					745					750		
Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met
		755					760					765			
Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	Asp	Pro	Glu	Met	Leu	Val
	770					775					780				
Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Asn	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu
785					790					795					800
Arg	Arg	Thr	Trp	Leu	Glu	Ser	Met	Ala	Lys	Ile	His	Ala	Arg	Asn	Gly
				805					810					815	
Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Ile	His	Ile	Ala	Ala	Leu	Ile
			820					825					830		
Ala	Glu	Tyr	Leu	Lys	Arg	Lys	Gly	Tyr	Trp	Lys	Val	Glu	Lys	Ile	Cys
		835					840					845			
Thr	Ala	Ser	Leu	Leu	Ser	Glu	Asp	Thr	His	Pro	Cys	Asp	Ser	Asn	Ser
	850					855					860				
Leu	Leu	Thr	Thr	Pro	Ser	Gly	Gly	Ser	Met	Phe	Ser	Met	Gly	Trp	Pro
865					870					875					880
Ala	Phe	Leu	Ser	Ile	Thr	Pro	Asn	Ile	Lys	Glu	Glu	Gly	Ala	Ala	Lys
				885					890					895	
Glu	Asp	Ser	Gly	Met	His	Asp	Thr	Pro	Tyr	Asn	Glu	Asn	Ile	Leu	Val
			900					905					910		

026
cont.

Glu Gln Leu Tyr Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr
 915 920 925
 Glu Leu Ile Ala Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys
 930 935 940
 Gln Arg Asp Phe Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg
 945 950 955 960
 Ser Tyr Leu Lys Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe
 965 970 975
 Gly Arg Tyr Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu
 980 985 990
 Glu Glu Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu
 995 1000 1005
 Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly
 1010 1015 1020
 Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys
 1025 1030 1035 1040
 Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro
 1045 1050 1055
 Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met
 1060 1065 1070
 His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser
 1075 1080 1085
 Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile
 1090 1095 1100
 Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val
 1105 1110 1115 1120
 Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp
 1125 1130 1135
 Glu Met Ser Arg Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu
 1140 1145 1150
 Glu Val Asp Met Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
 1155 1160 1165
 Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu
 1170 1175 1180
 Glu Thr Asn Ala Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys
 1185 1190 1195 1200
 Glu Ile Phe Arg Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val
 1205 1210 1215
 Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu
 1220 1225 1230
 Arg Ser His Tyr Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn

a26
 cont.

1235 1240 1245
 Glu Gln Ile Thr Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln
 1250 1255 1260
 Thr Cys Thr Arg Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val
 1265 1270 1275 1280
 Ser Ile Ser Ser Ser Ala Glu Val
 1285

<210> 23
 <211> 1220
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Human CLASP-3 protein

<400> 23
 Gly Pro Gly Pro Ala Arg Ser Thr Val Ser Ile Ser Leu Ile Ser Asn
 1 5 10 15
 Ser Ala Arg Val Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp
 20 25 30
 Ile Ser Gly Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile
 35 40 45
 Gly Ser Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly
 50 55 60
 Pro Lys Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser
 65 70 75 80
 Thr Gln Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu
 85 90 95
 Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys
 100 105 110
 Leu Phe His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser
 115 120 125
 Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met
 130 135 140
 Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala
 145 150 155 160
 Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala
 165 170 175
 Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp
 180 185 190
 Thr Glu Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn
 195 200 205
 Asp Leu Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys

Q26
 cont.

210					215					220					
Ser	Cys	Tyr	Lys	Gln	Val	Ser	Ser	Lys	Leu	Tyr	Ser	Leu	Pro	Asn	Pro
225					230					235					240
Ser	Val	Leu	Val	Ser	Leu	Arg	Leu	Asp	Phe	Leu	Arg	Ile	Ile	Cys	Ser
				245					250					255	
His	Glu	His	Tyr	Val	Thr	Leu	Asn	Leu	Pro	Cys	Ser	Leu	Leu	Thr	Pro
			260					265					270		
Pro	Ala	Ser	Pro	Ser	Pro	Ser	Val	Ser	Ser	Ala	Thr	Ser	Gln	Ser	Ser
		275					280					285			
Gly	Phe	Ser	Thr	Asn	Val	Gln	Asp	Gln	Lys	Ile	Ala	Asn	Met	Phe	Glu
	290					295					300				
Leu	Ser	Val	Pro	Phe	Arg	Gln	Gln	His	Tyr	Leu	Ala	Gly	Leu	Val	Leu
305					310					315					320
Thr	Glu	Leu	Ala	Val	Ile	Leu	Asp	Pro	Asp	Ala	Glu	Gly	Leu	Phe	Gly
				325					330					335	
Leu	His	Lys	Lys	Val	Ile	Asn	Met	Val	His	Asn	Leu	Leu	Ser	Ser	His
			340					345					350		
Asp	Ser	Asp	Pro	Arg	Tyr	Ser	Asp	Pro	Gln	Ile	Lys	Ala	Arg	Val	Ala
		355					360					365			
Met	Leu	Tyr	Leu	Pro	Leu	Ile	Gly	Ile	Ile	Met	Glu	Thr	Val	Pro	Gln
	370					375					380				
Leu	Tyr	Asp	Phe	Thr	Glu	Thr	His	Asn	Gln	Arg	Gly	Arg	Pro	Ile	Cys
385					390					395					400
Ile	Ala	Thr	Asp	Asp	Tyr	Glu	Ser	Glu	Ser	Gly	Ser	Met	Ile	Ser	Gln
				405					410					415	
Thr	Val	Ala	Met	Ala	Ile	Ala	Gly	Thr	Ser	Val	Pro	Gln	Leu	Thr	Arg
			420					425					430		
Pro	Gly	Ser	Phe	Leu	Leu	Thr	Ser	Thr	Ser	Gly	Arg	Gln	His	Thr	Thr
		435					440					445			
Phe	Ser	Ala	Glu	Ser	Ser	Arg	Ser	Leu	Leu	Ile	Cys	Leu	Leu	Trp	Val
		450				455					460				
Leu	Lys	Asn	Ala	Asp	Glu	Thr	Val	Leu	Gln	Lys	Trp	Phe	Thr	Asp	Leu
465					470					475					480
Ser	Val	Leu	Gln	Leu	Asn	Arg	Leu	Leu	Asp	Leu	Leu	Tyr	Leu	Cys	Val
				485					490					495	
Ser	Cys	Phe	Glu	Tyr	Lys	Gly	Lys	Lys	Val	Phe	Glu	Arg	Met	Asn	Ser
			500					505					510		
Leu	Thr	Phe	Lys	Lys	Ser	Lys	Asp	Met	Arg	Ala	Lys	Leu	Glu	Glu	Ala
			515				520					525			
Ile	Leu	Gly	Ser	Ile	Gly	Ala	Arg	Gln	Glu	Met	Val	Arg	Arg	Ser	Arg
	530					535					540				

Q26
cont.

Gly	Gln	Leu	Glu	Arg	Ser	Pro	Ser	Gly	Ser	Ala	Phe	Gly	Ser	Gln	Glu
545					550					555					560
Asn	Leu	Arg	Trp	Arg	Lys	Asp	Met	Thr	His	Trp	Arg	Gln	Asn	Thr	Glu
				565					570					575	
Lys	Leu	Asp	Lys	Ser	Arg	Ala	Glu	Ile	Glu	His	Glu	Ala	Leu	Ile	Asp
			580					585					590		
Gly	Asn	Leu	Ala	Thr	Glu	Ala	Asn	Leu	Ile	Ile	Leu	Asp	Thr	Leu	Glu
		595					600					605			
Ile	Val	Val	Gln	Thr	Val	Ser	Val	Thr	Glu	Ser	Lys	Glu	Ser	Ile	Leu
	610					615					620				
Gly	Gly	Val	Leu	Lys	Val	Leu	Leu	His	Ser	Met	Ala	Cys	Asn	Gln	Ser
625					630					635					640
Ala	Val	Tyr	Leu	Gln	His	Cys	Phe	Ala	Thr	Gln	Arg	Ala	Leu	Val	Ser
				645					650					655	
Lys	Phe	Pro	Glu	Leu	Leu	Phe	Glu	Glu	Glu	Thr	Glu	Gln	Cys	Ala	Asp
			660					665					670		
Leu	Cys	Leu	Arg	Leu	Leu	Arg	His	Cys	Ser	Ser	Ser	Ile	Gly	Thr	Ile
		675					680					685			
Arg	Ser	His	Pro	Ser	Ala	Ser	Leu	Tyr	Leu	Leu	Met	Arg	Gln	Asn	Phe
	690					695					700				
Glu	Ile	Gly	Asn	Asn	Phe	Ala	Arg	Val	Lys	Met	Gln	Val	Pro	Met	Ser
705					710					715					720
Leu	Ser	Ser	Leu	Val	Gly	Thr	Ser	Gln	Asn	Phe	Asn	Glu	Glu	Phe	Leu
				725					730					735	
Arg	Arg	Ser	Leu	Lys	Thr	Ile	Leu	Thr	Tyr	Ala	Glu	Glu	Asp	Leu	Glu
			740					745					750		
Leu	Arg	Glu	Thr	Thr	Phe	Pro	Asp	Gln	Val	Gln	Asp	Leu	Val	Phe	Asn
		755					760					765			
Leu	His	Met	Ile	Leu	Ser	Asp	Thr	Val	Lys	Met	Lys	Glu	His	Gln	Glu
	770					775					780				
Asp	Pro	Glu	Met	Leu	Ile	Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Gly	Tyr
785					790				795						800
Gln	Thr	Ser	Pro	Asp	Leu	Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Gly
				805					810					815	
Lys	His	Ser	Glu	Arg	Ser	Asn	His	Ala	Glu	Ala	Ala	Gln	Cys	Leu	Val
			820					825					830		
His	Ser	Ala	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Ser	Met	Leu	Glu	Asp	Arg
		835					840					845			
Lys	Tyr	Leu	Pro	Val	Gly	Cys	Val	Thr	Phe	Gln	Asn	Ile	Ser	Ser	Asn
	850					855					860				

926
cont.

Val Leu Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu
 865 870 875 880
 Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly
 885 890 895
 Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu
 900 905 910
 Ala Val Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn
 915 920 925
 Arg Asp Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala
 930 935 940
 Phe Ser Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly
 945 950 955 960
 Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp
 965 970 975
 Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu
 980 985 990
 Ile Ser His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp
 995 1000 1005
 Val Val Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu
 1010 1015 1020
 Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe
 1025 1030 1035 1040
 Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr
 1045 1050 1055
 Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg
 1060 1065 1070
 Ala His Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr
 1075 1080 1085
 Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His
 1090 1095 1100
 Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met
 1105 1110 1115 1120
 Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala
 1125 1130 1135
 Asp Pro Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr
 1140 1145 1150
 Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile
 1155 1160 1165
 Pro Ser Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys
 1170 1175 1180
 Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys

026
 cont.

225					230					235					240
Val	Leu	Gln	Lys	Ser	Arg	Asp	Val	Lys	Ala	Arg	Leu	Glu	Glu	Ala	Leu
				245					250					255	
Leu	Arg	Gly	Glu	Gly	Ala	Arg	Gly	Glu	Met	Met	Arg	Arg	Arg	Ala	Pro
			260					265					270		
Gly	Asn	Asp	Arg	Phe	Pro	Gly	Leu	Asn	Glu	Asn	Leu	Arg	Trp	Lys	Lys
		275					280					285			
Glu	Gln	Thr	His	Trp	Arg	Gln	Ala	Asn	Glu	Lys	Leu	Asp	Lys	Thr	Lys
	290					295					300				
Ala	Glu	Leu	Asp	Gln	Glu	Ala	Leu	Ile	Ser	Gly	Asn	Leu	Ala	Thr	Glu
305					310					315					320
Ala	His	Leu	Ile	Ile	Leu	Asp	Met	Gln	Glu	Asn	Ile	Ile	Gln	Ala	Ser
				325					330					335	
Ser	Ala	Leu	Asp	Cys	Lys	Asp	Ser	Leu	Leu	Gly	Gly	Val	Leu	Arg	Val
			340					345					350		
Leu	Val	Asn	Ser	Leu	Asn	Cys	Asp	Gln	Ser	Thr	Thr	Tyr	Leu	Thr	His
		355					360					365			
Cys	Phe	Ala	Thr	Leu	Arg	Ala	Leu	Ile	Ala	Lys	Phe	Gly	Asp	Leu	Leu
	370					375					380				
Phe	Glu	Glu	Glu	Val	Glu	Gln	Cys	Phe	Asp	Leu	Cys	His	Gln	Val	Leu
385					390					395					400
His	His	Cys	Ser	Ser	Ser	Met	Asp	Val	Thr	Arg	Ser	Gln	Ala	Cys	Ala
				405					410					415	
Thr	Leu	Tyr	Leu	Leu	Met	Arg	Phe	Ser	Phe	Gly	Ala	Thr	Ser	Asn	Phe
			420					425					430		
Ala	Arg	Val	Lys	Met	Gln	Val	Thr	Met	Ser	Leu	Ala	Ser	Leu	Val	Gly
			435				440					445			
Arg	Ala	Pro	Asp	Phe	Asn	Glu	Glu	His	Leu	Arg	Arg	Ser	Leu	Arg	Thr
	450					455					460				
Ile	Leu	Ala	Tyr	Ser	Glu	Glu	Asp	Thr	Ala	Met	Gln	Met	Thr	Pro	Phe
465					470					475					480
Pro	Thr	Gln	Val	Glu	Glu	Leu	Leu	Cys	Asn	Leu	Asn	Ser	Ile	Leu	Tyr
				485					490					495	
Asp	Thr	Val	Lys	Met	Arg	Glu	Phe	Gln	Glu	Asp	Pro	Glu	Met	Leu	Met
			500					505					510		
Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Ser	Tyr	Gln	Ala	Ser	Pro	Asp	Leu
		515					520					525			
Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Glu	Lys	His	Thr	Lys	Lys	Lys
	530					535					540				
Cys	Tyr	Thr	Glu	Ala	Ala	Met	Cys	Leu	Val	His	Ala	Ala	Ala	Leu	Val
545					550					555					560

a26
cont.

Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro Val Gly
 565 570 575
 Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Val
 580 585 590
 Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys Ala Gly
 595 600 605
 Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala
 610 615 620
 Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu Val Tyr
 625 630 635 640
 Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg Lys Leu
 645 650 655
 Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp Ser Ile Val Asn
 660 665 670
 Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Phe
 675 680 685
 Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu
 690 695 700
 Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg Leu Glu Ala Phe
 705 710 715 720
 Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val Ile Lys Asp Ser
 725 730 735
 Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
 740 745 750
 Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu Met Lys Asp Arg
 755 760 765
 Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg Phe Met Tyr Thr
 770 775 780
 Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu Leu His Glu Gln
 785 790 795 800
 Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile
 805 810 815
 Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro
 820 825 830
 Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
 835 840 845
 Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met Leu Gln Met Val
 850 855 860
 Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly Pro Leu Glu Val
 865 870 875 880

a2b
 cont.

Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro Lys Leu Tyr Arg
885 890 895

His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe Ile Met Arg Cys
900 905 910

Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp Gln Arg
915 920 925

Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys Glu Asn
930 935 940

Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys Pro Ile
945 950 955 960

Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser Ser Phe
965 970 975

Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
980 985

<210> 25
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from CLASP-1

<400> 25
Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 26
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from CLASP-2D KIAA1058

<400> 26
Phe Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp
1 5 10 15

Ser Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu
20 25 30

Tyr Ile Tyr Lys Glu Pro
35

<210> 27
<211> 14

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motif B from CLASP-2

<400> 27

Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
1 5 10

<210> 28

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from CLASP-6

<400> 28

Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 29

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from CLASP-4

<400> 29

Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 30

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from DOCK180

<400> 30

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 31
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from DOCK2

<400> 31
Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn
1 5 10 15
Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 32
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from DOCK3

026
cont.
<400> 32
Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15
Lys Glu Tyr Val Cys Arg Gly His
20

<210> 33
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from KIAA0716

<400> 33
Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15
Lys Glu Phe Val Cys Arg Gly His
20

<210> 34
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from CLASP-3

<400> 34
Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
1 5 10 15

Glu Phe Val Tyr Lys Glu Pro
20

<210> 35
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motif C from rat TRG

<400> 35
Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15
Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser
20 25 30
Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln
35 40 45
Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
50 55 60

a26
ent.

<210> 36
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motif C from CLASP-1

<400> 36
Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15
Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser
20 25 30
Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln
35 40 45
Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu
50 55 60

<210> 37
<211> 60
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motif C from CLASP-2

<400> 37

Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15

Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
35 40 45

Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
50 55 60

<210> 38

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motif C from CLASP-4

<400> 38

Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu
1 5 10 15

Tyr Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser
20 25 30

Asp Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln
35 40 45

Val Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu
50 55 60

<210> 39

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motif C from CLASP-3

<400> 39

Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe
1 5 10 15

Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser
20 25 30

Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
35 40 45

Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu
50 55 60

<210> 40
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motif C from KIAA0716

<400> 40
His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu
1 5 10 15
Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr
20 25 30
Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
35 40 45
Ile Pro Glu Ser Gln Glu
50

<210> 41
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motif C from DOCK3

<400> 41
His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu
1 5 10 15
Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala
20 25 30
Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
35 40 45
Ile Pro Asp Tyr Val Asp
50

<210> 42
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motif C from DOCK2

<400> 42
Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn
1 5 10 15

Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr
20 25 30

Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asp Glu His Pro
35 40 45

<210> 43
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motif C from DOCK180

<400> 43
Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe
1 5 10 15

Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val
20 25 30

Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val
35 40 45

Leu Asp Glu His Pro
50

a26
und.
<210> 44
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs D and E from CLASP-1

<400> 44
Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val
20 25 30

Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn
35 40 45

<210> 45
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs D and E from rat TRG

<400> 45
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg

1 5 10 15
 Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu His
 35 40 45

<210> 46
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from CLASP-2D KIAA1058

<400> 46
 Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
 35 40 45

<210> 47
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from CLASP-2

<400> 47
 Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
 35 40 45

<210> 48
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from CLASP-6

<400> 48
 Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

His Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
 35 40

<210> 49
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from CLASP-4

<400> 49
 Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val
 20 25 30

Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln
 35 40 45

Q26 cont.
 <210> 50
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from CLASP-3

<400> 50
 Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg
 1 5 10 15

Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val
 20 25 30

Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala
 35 40 45

<210> 51
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from CLASP-5

<400> 51
 Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg
 1 5 10 15

Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro Ile Glu Val
 20 25 30

Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
 35 40 45

<210> 52
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from KIAA0716

<400> 52
 Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp
 1 5 10 15

Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn
 20 25 30

Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys
 35 40 45

<210> 53
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from DOCK2

<400> 53
 Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1 5 10 15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20 25 30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35 40 45

<210> 54
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from DOCK3

<400> 54
 Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp
 1 5 10 15

Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn

20 25 30

Ala Ile Gln Val Val Glu Asn Lys Asn Gln Glu Leu Arg
 35 40 45

<210> 55
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from DOCK180

<400> 55
 Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1 5 10 15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20 25 30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35 40 45

<210> 56
 <211> 58
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs F and G from CLASP-1

<400> 56
 Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala
 1 5 10 15

Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys
 20 25 30

Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln
 35 40 45

Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp
 50 55

<210> 57
 <211> 58
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs F and G from rat TRG

<400> 57
 Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
 1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 58

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-2D KIAA1058

<400> 58

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 59

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-2

<400> 59

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 60

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-6

<400> 60

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 61

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-3

<400> 61

Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
20 25 30

Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
35 40 45

Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg
50 55

<210> 62

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-4

<400> 62

Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser
20 25 30

Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys
35 40 45

Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu
50 55

<210> 63
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-5

<400> 63
Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln
1 5 10 15
Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp
20 25 30
Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu
35 40 45
Phe Ile Met Arg Cys Gly Glu Ala Val Glu
50 55

Q26
cont.
<210> 64
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from KIAA0716

<400> 64
Pro Leu Thr Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
1 5 10 15
Gly Val Ser Arg Tyr Gln Glu Ala Phe Phe Val Lys Glu Tyr Ile Leu
20 25 30
Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met
35 40 45
Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala
50 55 60

<210> 65
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from DOCK2

<400> 65
Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly

1 5 10 15
 Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
 20 25 30
 Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile
 35 40 45
 Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys
 50 55 60

<210> 66
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs F and G from DOCK3

<400> 66
 Leu Leu Ser Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
 1 5 10 15
 Gly Ile Ala Arg Tyr Gln Glu Ala Phe Phe Asp Lys Asp Tyr Ile Asn
 20 25 30
 Lys His Pro Gly Asp Ala Glu Lys Ile Thr Gln Leu Lys Glu Leu Met
 35 40 45
 Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala
 50 55 60

<210> 67
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs F and G from DOCK180

<400> 67
 Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
 1 5 10 15
 Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
 20 25 30
 Asp His Pro Glu Ala His Glu Lys Ile Glu Lys Leu Lys Asp Leu Ile
 35 40 45
 Ala Trp Gln Ile Pro Phe Leu Ala Glu Gly Ile Arg
 50 55 60

<210> 68
 <211> 683
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 1.1
sequence of bacterial artificial chromosome BAC4
using primer HC2AS2

<220>

<221> modified_base

<222> (1)..(683)

<223> n is g, a, c, or t

<400> 68

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gacaaagttt gcaccatttt gcaagaagaa aaaaatccta atgtgttata ttactatatt 120
tttactctat agatcttttt ctaaagaaag aaagtacaac tgaagtgctt atatgtattc 180
atataaatga ctagtacaag catcattttg caacagattt cccctttcat tggaggatct 240
tcttgatgtt atttgtacac gatcaatttt tagtcttaat aagatgaggc tgggtgtggt 300
ggctcacacc tgtaatccta gcatttttga ggccaagggtg ggcagatcac tttagcccag 360
gggtttgaga ccagcctggc caacatggca aaaccttgtc tctacaaaaa tacnaaaatt 420
atccaggcat ggtgatgtgt gcctgtagtc ccaactncct aggaggctag gggtaggggg 480
atttgcaaga ggctgggagg gtcaaagccc naantgagcc attggtncat gtcacttgga 540
ccccaagcnn gggnganca agagcaaagg actnntgtnn tttanaaaaa aaaccgggct 600
accatacnaa ccaaccncn nacctaccn acctttccan nttaaaanaa ggctttgnct 660
tgcanaggaa aancaaaatn ncc 683
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<210> 69

<211> 673

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 1.2
sequence of bacterial artificial chromosome BAC26
using primer HC2AS2

<220>

<221> modified_base

<222> (1)..(673)

<223> n = g, a, c, or t

<400> 69

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tctggtttct acagtgtata ctnaggtatg tgctccttna acaaaattag cagttgctgc 60
tctgtgacaa agtttgcacc attttgcaag aagaaaaaaa tcctaattgtg ttatattact 120
atatttttac tctatagatc tttttctaaa gaaagaaagt acaactgaag tgcttatatg 180
tattcatata aatgactagt acaagcatca ttttgcaaca gatttcccct ttcattggag 240
gatcttcttg atgttatattg tacacgatca atttttagtc ttaataagat gaggctgggt 300
gtgggtggctc acacctgtaa tcctagcatt ttggaggcca aggtgggcag atcactttag 360
cccagggggtt tgagaccagc ctggccaaca tggcaaaacc ttgtctctac aaaaatacaa 420
aaattatcca ggcatgggtga tgtgtgcctg tagtcccagc tacctaggag gctagggtag 480
ggggattgca agaggctngg aggtcaaggc ccgcagttag ccatggtcac gtcactgcac 540
ccccagccag ggccgacagg agcaagactn ttgtntcaaa aaaaaacagn aaccaacanc 600
caacaacaac aacnaccttt cngcaaaana agcttgctnc aangaaacca aaatgncttc 660
ttnttttccc ccn 673
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<210> 70

<211> 1034

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 1.3
 sequence of bacterial artificial chromosome BAC6
 using primer HC2AS2

<220>
 <221> modified_base
 <222> (1)..(1034)
 <223> n = g, a, c, or t

<400> 70
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 aaaatcctaa gtgtnatata actatatnnn tactctatag atcttntcta aagaaagaaa 180
 gtcaactgat gtgcttatata gtatncatat aaatgactag tacatgcata attttgcaac 240
 agatntctcc tcacattgga ggatcttctn gangnattcg acacgatnan tattagtctn 300
 aataagatga ngctgggtgtg gnggtacact gnatctagca tntggangca tgtggcagac 360
 acttancnc ggtngagaca gctgtcactg ncnaactgtc tctntaaanc aaannctccg 420
 cnggngatgg gctgagccag tcctagnngc tagntagnga tgnngagntg tngcacgncg 480
 agngagcatg ntctgtactg actcatcagg cgnacacag ntctgttcna aaacatacca 540
 cacacactcn cacctnccga aaattgctct nnaaanatgc ttntttcaca cngntncaat 600
 cnctatatnn tcttctatcc tncnacgtnt nattannatc ttncnctgca naacnatncc 660
 nccacctnna nnaccttang cttngtttca cgcttatagc tcccctacac ntncnagcnn 720
 ttncnngtga agggccnccc gaactctacg ncataactct tccgtatatn gcctcgggtca 780
 ncgccatctg ctgtntnctc ntcnctngcn ntnancngt ncgctatctc tnnnccggat 840
 ccncccata tntnntctct acttanagcg taanntntnc ncncactant cacaacttnt 900
 ncntnnaact ctatctnctc ctctctacca cctcacttac tacctnttca cncantctcc 960
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 tctacgctnn ntnt 1034

<210> 71
 <211> 644
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 2.1
 sequence of bacterial artificial chromosome BAC4
 using primer HC2S1

<220>
 <221> modified_base
 <222> (1)..(644)
 <223> n = g, a, c, or t

<400> 71
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 ttgaccttct tagaactgca cactctattg cactgtacag atttcaggat ggctgcaggg 180
 attgatttga aaactaagga cacatttcaa taaacaatgt cttcaattga tttttagggc 240
 tcctcctact tcaatgaagg acttcaggta gcttataatt acagacacag gctcaataca 300
 ataaaaaaat tagtaaggca gagcttttaa aaaaaaaaag gaaaaagata attctaccag 360
 agaaaggcta catggtgact tctgttacca gtaacaaccc ccgcactacc tttgggtctc 420
 caggagcaaa acagctaatt tagttgttga tctgcttgaa gacaaagccc ctgtccatga 480
 aggtgaaaca tctctgtgga ggaaaacaag caaaaaagtt atttcaggtc caaacatttc 540
 ggaaatttgg attcaaagca ggcatttatt gctaataagt ttatccactg acataaaaaa 600
 catgccttca acattgccag agcacctact ctattntagt cncn 644

<210> 72
<211> 725
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 3.1
sequence of bacterial artificial chromosome BAC4
using primer C96AS

<220>
<221> modified_base
<222> (1)..(725)
<223> n = g, a, c, or t

<400> 72
aatcagcaga ccaaacagag gcaggtagag ggtggctatc cttgcctgat ggctctgaaa 60
agaagacaca catggtaagt ttgacccagg attctgagaa ccgaactaag ttggtgctga 120
ccatctcctt tatttggatc cttcctataa agacagatat ttgatttttag tcccaaaata 180
gagcaaaatc ttagtgctgt taccatgaat tttctaactg attactttct ttacaccact 240
taaaataaag gacattatca atgcacattc cttccattgg ggaccactca cccttgaagc 300
atatctgtca tcaaaagaat gctttatcag caggttcttg agcacactga tggcgatcag 360
acggacctcc cggaactcct ggagggctgt cccacactcc ctnagtaaca gtcccaccaa 420
gaagtgggtt ctgcagaact catctgttaa tgagtagtca agctgggagg tctgaaatga 480
ggatagaaac tactttgngt taggaaagat gcaatgctct tttgaataaa acaaacaaac 540
caaacnaaca aaaaaaaaaac taagacccat ccttntgnat ttcaagccca ccctggggtn 600
ggtcaaagag atgatcagna ntttggcntt naaatgaaga aagaaatnaa ttntccaggg 660
gntgttctnc ttttttagcac anggagggat nttaantgaa aaccaattta aatccaattn 720
agng 725

Q26
cont.
<210> 73
<211> 689
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 4.1
sequence of bacterial artificial chromosome BAC4
using primer C2AS5

<220>
<221> modified_base
<222> (1)..(689)
<223> n = g, a, c, or t

<400> 73
ttcctttctg caaggctgtt cccgaatctg tgcttatgag agatcctctc gaatcagcat 60
ttctcacact gttgatgttt ggagttgagg ttgtatatgg agaagctaaa tggaaatcaa 120
gccaacaata aagttttatt aagacagaac aaaataaaga tgagtactga actttaaggg 180
aaattgcttt tattgcactt attttttctg ttaggaagtt ggctcaagag ttgcattcca 240
ttacttcacc tttaaagaac caggtcatat acaatgagat aaaaagaaac tagtctgaaa 300
cattcagatg taaacatcaa ttcacttggt agaaaccacc tttgatcgct aaagactaaa 360
tgcatacctg tttcagaatg tgatagaatg aagacttaaa aaaattaaaa gataaatcca 420
cctacaacta tcaaatcaca aaattaaacc acacaacaaa cttgtagcat tcaaactggg 480
aataaacact gaggagccta cccaactctg aggggtgtca tgggggtattt taaattttcg 540
aggagaacac agtgatatgt gacctcagcc agaagctgct gtttnagcag caggttggtg 600
ctatgctcct ttttgaagac atatttgtga agctgggtat tttggggggc ctgcttatga 660
taaaanggca aggtnttcaa tgnaggggn 689

<210> 74
<211> 680
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 4.2
sequence of bacterial artificial chromosome BAC26
using primer C2AS5

<220>
<221> modified_base
<222> (1)..(680)
<223> n = a, g, c, or t

<400> 74
ttcctttctg gaaggctggt acccgaatct gtgcttatga gagatcctct cgaatcagca 60
tttctcacac tgttgatggt tggagttgag gttgtatatg gagaagctaa atggaaatca 120
agccaacaat aaagttttat taagacagaa caaaataaag atgagtactg aactttaagg 180
gaaattgctt ttattgcact tattttttct gttaggaagt tggctcaaga gttgcattcc 240
attacttcac ctttaaagaa ccaggtcata tacaatgaga taaaaagaaa ctagtctgaa 300
acattcagat gtaaacaatca attcacttgt tagaaaccac ctttgatcgc taaagactaa 360
atgcatacct gtttcagaat gtgatagaat gaagacttaa aaaaattaaa agataaatcc 420
acctacaact atcaaatcac aaaattaaac cncacaacaa acttgtagca ttcaaactgg 480
taataaaaca ctgaggagcc taccacaact tgaggggtgt caatggggtn tttttaaatt 540
tttcgnggga nanccagtg ntatggtgac cttcacccaa gaagcttggt tgtttnacca 600
agcnaggttg nncntngctc ctttttagaa nacnntattt tnnnaaatnc tggntttttt 660
nngnggcccc ctncnttnt 680

Q26
ant
<210> 75
<211> 686
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 5.1
sequence of bacterial artificial chromosome BAC4
using primer C2S6

<220>
<221> modified_base
<222> (1)..(686)
<223> n = g, c, a, or t

<400> 75
ttcctggata aggtaattgc ttttacccaa cacaaatggt tcttataatc aatggattta 60
gccc aaagta aacgtacttc atgttctagt gcctttttaag tgtgacctt tgtttttttc 120
taaaccaccc ggctgacctg gagtaggtga tgagagcttt aagggtgggg cccattcctt 180
gaagtgtctt gattcctggt tccagtagct cagatcctgg gcagggtttg cagtggagcg 240
tcttgagtga atggctctgg tgggttgaac ggggaggagc tcaaaatgct gccatctca 300
atttctgtga gtctttttat ttattttatt attttttgag acagagtctc gctctgtcgc 360
ccaggctgga gtacagcggc acgatctcaa ttnactgcaa cctccgcctc ctgggttcaa 420
acgactcctc tgcctcagcc tccccagcag ctgggaccac aggcacaagc caccaccgcc 480
cggctaattt tttgtntttt tagtagagat ggggtttcac catatttggc caggctgggc 540
tcaaactcct gacctcgtca tccgcncct cggncncca aagtgttgg gattncaggc 600
ngtgagccca cttacacctn gggcaattcc ctgtnagtct tttttaccag agacaccatc 660
attcaacaca gctttttccac ccacaa 686

<210> 76

<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 5.2
sequence of bacterial artificial chromosome BAC26
using primer C2S6

<220>
<221> modified_base
<222> (1)..(672)
<223> n = g, a, c, or t

<400> 76
tgagaagagc aatttcctgg ataaggtaat tgcttttacc caacacaaat gtttcttata 60
atcaatggat ttagcccaaa gtaaacgtac ttcattgttct agtgcctttt aagtgtgacc 120
ttttgttttt ttctaaacca cccggctgac ctggagtagg tgatgagagc tttaagggtg 180
gggcccattc cttgaagtgc tctgattcct gtttccagta cctcagatcc tgggcagggt 240
ttgcagtggg gcgctcttgag tgaatggctc tgggtgggtg aacggggagg gactcaaaat 300
gctgcccatt tcaatttcct gtagtctttt tatttattta tttatttttt gagacagagt 360
ctcgctctgt cgcccaggct ggagtacagc ggcacgatct caattcactg caacctccgn 420
ctccctgggt tcaaacgact cctctgnctn agnctcccag cagcctggga accacaggct 480
cangccacca cgcccggcta attnttgtaa ttttnagtaa naaattgggg gttctcacca 540
tnttggecca agncttgggc ctaaaaacct tncnaccnt cgnattcnc ncccnaccn 600
tgggcncctn tcaaangngc ttggggattt ancanngcn ttaaccccc ntatcacctg 660
ggnccttaat tt 672

<210> 77
<211> 700
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 6.1
sequence of bacterial artificial chromosome BAC4
using primer C2S7

<220>
<221> modified_base
<222> (1)..(700)
<223> n = g, a, c, or t

<400> 77
nagngngggg ttnagnctgt tgaagcctgn nacngnggtgn gtgctngaac tctgtgggct 60
ttcaggtact ggggtatctg ggagcctgct gtttgcatg ctagtgcac agaccagggc 120
tttttcctcc ctgtagctgc tacttataca catagctcta actgagatga ttctccagac 180
aactgatgca gagcagcaaa agcttctgcc gttctcccct tctaggagtg tctcctttct 240
ttggaaagag atcatgaggg gctagattgt aatgaagtga ggctcagtgc ttgagcacat 300
ccggtaaaaag ttccaatata ttggtcataa agtttctcat tctttatagc agttaatttc 360
tctggctcat gagttttctt agtttttaac tgacttttaa attaatgtct ccagcaccag 420
tcatatcccc agggcaaact caaaggcatg agaggccaga ctcggtcctt ggtcatagca 480
accctgtctt agggccttgg tccctgcctc cgcttgtgtg ctgtggcgca ggtcctatgg 540
gcccttagga aacaggacca ccctgtcgca cccctacag agaccagcca agtttgacat 600
tagatcaccg tagcaatgtn tgcaaattcc agtttcttgc taaaacagg taagccttgc 660
agccacttta tctgtaactg gcngagggtt tgacataaaa 700

<210> 78
<211> 676

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 7.1
sequence of bacterial artificial chromosome BAC4
using primer C2S8

<220>

<221> modified_base

<222> (1)..(676)

<223> n = g, a, c, or t

<400> 78

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ctctcgacac gctgttttcta ttaacattgg cgtttaaggt ttgtatcaat ttgctgttcg 60
nggttctagt tttacctttc acattcattc tgcttggtta gctcagttag cacaacttta 120
ctatgttgca tttttacttc agcaattatt tttgtccctg taaggaaacc attaatcttt 180
aaattccttt aatgaaatca ttccacagtg aatggcttga atgccctgaa ataaaattta 240
actggtcagt gtgtgctgcg cgcttgggta tgggtggaaac acggtctctg gaggcagtta 300
actcttggct cgaaccttga ggatgggtgaa tataggcacc taatcaggca tttctgcctt 360
gaatatcttt aaatatatcc aaatggtata gcgtttaatt agatttttat gtagaaagga 420
gcaataaaca caagacacat gttttcagtt ttttatctgt tactgcatta aatgataaaa 480
acgttttgga gatagaaaat gaaaggggtt ttttttttgt cttgttttaa agtttttagca 540
aataatatcc aagtaggtgg agatggactc ttcaccactc tcctgttttt aggaacccaa 600
tactttttca ttcttgctaa atgattactt ccattttctag catagaaaag gagaaaattg 660
gaatgagtgt ttatat                                     676
```

<210> 79

<211> 686

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 8.1
sequence of bacterial artificial chromosome BAC4
using primer C2S9

<220>

<221> modified_base

<222> (1)..(686)

<223> n = a, c, g, or t

<400> 79

```
cgctttnaaa tnccagccgc tactgcgggg cgntnaattc gaaacgtggt gttntctgtg 60
atgcctggct ctgattgtgt gggattggtc atcagtggcg gttggcagnt ggggttcatg 120
gaagcggcca tggggactga tggcaggccc ttggattgcc accgcagagc ctggcagtgt 180
ctttgggtctg cattcctacc ggcgaagtct catttcacct cacgtgttat ctcttgga 240
gcattccttt agcgggctgt gtctaccctt ccatectctc gtccaaactc cccctccttc 300
tctgttctgt ctcttccca tctcttctc cccagtctct ctctctatgt tcttctctca 360
gtgggtttctc ttcctctggt tgactttcca aggtcatttt gactgttctt gctcccaact 420
acaaagatac taaaatctca cctaaccact cttcttcttt cttaatgaaa gaatgttttc 480
agtccatccc aaatttgtgt ggacttcaca aaccttctct aaaatggagc cttttctctt 540
cctactcttg actagntggg aaacgctcca tggtcttggc cagaactccc tgggtgagtag 600
cgtcactccc actttcctgt gcagaaccaa gcctcctaga aaactccttt gcanctgagt 660
gggttgggac acgccctttn tttggg                                     686
```

<210> 80

<211> 680

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 9.1
sequence of bacterial artificial chromosome BAC4
using primer C2AS10

<220>

<221> modified_base

<222> (1)..(680)

<223> n = g, a, t, or c

<400> 80

```
tttanaccna tntatccgng tcagttanag gagtctctga gaaatttccg acagcgggtgt 60
gagtttgggt tccttgtaaa tatactcctt tccatcttca tcttcaaaga atccctgtga 120
cataaagcac aattagagct atccctgaac gtaagcccag ggcttaccac ctaggaagcg 180
ttcttttatt acaaggggga aaaaaaggaa tgggtctaaa aatccagctg aaatgggctt 240
tctgaatgag aaagaaaatg ctaataacat gaagtctagg tgcaaaggta aaggaaaaac 300
acaacattgc aaacttattc aagaatgcag tcattaagtg ttgagtgaag tgaaagattt 360
tgatacaag actaagctgt cccagggaag tctaattgga gtcaagcctg tttcactttc 420
ccaagaagca gaactcacta naaaatgatg agcagcccac gacaggcagg ctcagaagtg 480
gacatgcctc ccttctcctg atggctncca tgcacacagg attttatggc atgaactgaa 540
gcgtttgggg gtctggagta agtttagtaa aagttaggta aagcttgtat aaattgtatt 600
tttgctttac ccgatgagaa aaaaaatatt naagacctgg tagcttcaat attcaagaaa 660
aatatttttc atntcaccgc 680
```

<210> 81

<211> 619

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 10.1
sequence of bacterial artificial chromosome BAC4
using primer C2S11

<220>

<221> modified_base

<222> (1)..(619)

<223> n = g, a, c, or t

<400> 81

```
ngnangtgga gccncgancc agggacaatc tnaacctnct taaactgtac tcggatnaat 60
ttgggttctga aaatgtcaaa atgatacagg attctggcaa ggtattgacc atgtttggan 120
aagtttcata gcaatgtaat gttgtgatnc gattacatat natatatatt taaatgtnta 180
tagaaaaaaa cacangaaaa atattaagga ttggtggccc gtgagtggca ggtgtatntt 240
cttnctgac ctttagngct ttccattaca tgcntgacat taaaaaaanc tttatcgcct 300
aatttttgaa acatctaatt ttacaaaata attaaccgtn tggccangna tattntcatt 360
tttaggncca gctatttaga aactctgaca naaatgaggg gctgtggcct ncctncctnn 420
acttgnccct ctttcnngna tgtaccacat gaacttgncc cctctttcnn ctnaccgggt 480
ggcatgttan aggacaggtt gaaaccncan tngggcngga ntnnggttna attgggacac 540
aatggtaacna ngctctatng gaatngaaac tctcccnacn nncngtgnnc cntggggaaa 600
atngnncnna ttcattttt 619
```

<210> 82

<211> 597

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 11.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2S12

<220>
 <221> modified_base
 <222> (1)..(597)
 <223> n = g, a, c, or t

<400> 82
 agnanngttn ngcagctgca nntctggacc canaggccgc angggcacga gccnggacac 60
 gctcggcaaa gagctgtcca gagggattca gaagcttcag gactggaagg gtcttttcgag 120
 ctcaagttagc cacccccaca cccatttcag tttcacattt atctagtgtc tccttttgaa 180
 tacttgggat gtttttctgt tgatctgttg gcacttcctt cttccacaag accagaagct 240
 catatccaat ctaaggtcac ttacccttct gagaatctga tgaaaatggc gtgccttatg 300
 tgcctagatg cttttgcaca cagtctaagg tgacttatgg actccaggtc cagcagccac 360
 acccagtcct gggctctccg acagggaggg acccgtcttc acacacctgt ctcaggttct 420
 agcattgggc tgcttcagcg gtctcaggct gtgagtaaat gggatgtgag cttggatcgc 480
 cccacgctgt tgncccccg ggggcttggc cagctggcca cttngaaatg cctccttttg 540
 cccaggaaag ctcaactgcat ttcaatgggg nttntccacg aagttcanct ttanggg 597

<210> 83
 <211> 634
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 12.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2S13

<220>
 <221> modified_base
 <222> (1)..(634)
 <223> n = a, c, g, or t

<400> 83
 agnaaggtnn ctcantnaan ncagcgtgag ngttcagggt agccaggcac agcaggcccg 60
 agggcagcag gggacgtcct tgcccctggg tgacttgaga gtcgtttcca ctaacaaggt 120
 ctacttgaga gcctcgggtt accaagtgat ccctgctccc tccccccaac gtntgtgaca 180
 tttctcctga tatcagaggg ggaggaaacc tcatgatccc tgccccccgc cccatgagga 240
 ctgactgtgg ggacaaagag ccagatctca tagactacce tgatttgtca gtatttgagg 300
 aattctgggt gcctgattag aagcatcaag actcttctaa atncaaagaa gtgtggagag 360
 cagtagattt tcctataaaa ctggtgttgc tggtttctat gaaaattgga tccaaaaaaa 420
 gtccttaagt ttaccctctt aatggnatct tttgattaat ggaattcatt attttaatat 480
 agcccaatca atccaatttt tctttatttg tagcattttt atgttctctt taaaaaaatc 540
 ttggnctacc tccaaaattt cacagatgtt ctccatagggt tttcctcctt ttgggttcaag 600
 catcccatc aangtcttgc agtccattct gggg 634

<210> 84
 <211> 567
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 13.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2S14

<220>
 <221> modified_base
 <222> (1)..(567)
 <223> n = a, g, c, or t

<400> 84
 gacttanatt tattcttcct tgcagagtag tgtagaata gatggcctac agaaaaaaaa 60
 gggtctggga tctacatggc agggagggct gcactgacat tgatgcctgg gggacctttt 120
 gcctcgaggc tgagctggaa aatcttgaaa atattttttt ttctctgtgg cacattcagg 180
 ttgaatacaa gaactatatt tgtgactatg tttttgatga cctaagggaa ctgaccattg 240
 taatttttgt accantgaac cangagattt aagtgccttt atattcattt ccttgcattt 300
 aagaaaatat gaaagcttaa ggaattatgt gagcttaaaa ctagtcaagc antttagaac 360
 caaaggccta tnttnataac cgcaactatg ctnaaaagna caaagtagta cagnatattg 420
 ntatgtacat atcatttggg aatacacncc nggcnttctg tacatatatg tattacattt 480
 ctacnttttt aatactcccn tgggcttatg ccnttaaggt taanttgnga taaatttngg 540
 ctgttcnngt ntatncnata cncctttt 567

<210> 85
 <211> 662
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 14.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2AS15

a76
 end.

<220>
 <221> modified_base
 <222> (1)..(662)
 <223> n = a, c, g, t

<400> 85
 atgagaatgt aatacatata tgtacagaat gccaggactg tattaacaat gatatgtaca 60
 taacaatata ctgtactact ttgtactttt cagcatagtt gcggttatta atataggcct 120
 ttggttctaa actgcttgac tagttttaag ctcacataat tccttaagct ttcataattt 180
 cttaaagtga aggaaatgaa tataaaagca ctaaactctc tggttcactg gtacaaaaat 240
 tacaatggtc agttccctta ggtcatcaaa aactagtcac aaaaatagtt cttgtattca 300
 acctgaatgt gccacaggaa aaaaaaata ttttcaagat tttccagctc agcctcgagg 360
 caaaaggccc ccaggcatca atgtcagngc agccctcctg ccatgtagat cccagaacct 420
 tttttttctg taggccatct attctaacac tactctgcag ggagaataaa atctaaagnc 480
 cagctcaaga gtgctaccac acctttgtta agacacaatg aaaacttttg atattggcag 540
 gngagattta aaaaaaatg tgccctttct taccactcct atagnaaagt ctgggttaaga 600
 aataaccgtt ggtctttatt ttccttttnt ttccccttcc cttgggnctt cctggggctc 660
 gg 662

<210> 86
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: KV1.3
 inhibitor

<400> 86
 Thr Thr Asn Asn Asn Pro Asn Ser Ala Val Asn Ile Lys Lys Ile Phe
 1 5 10 15

Thr Asp Val

<210> 87
<211> 4898
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (567) .. (4148)

<220>
<223> Human CLASP-2

<400> 87
aattgtaata cgactcacta tagggcgaat tgggtaccgg gccccccctc gaggtcgacg 60
gtatcgataa gcttgatata gaattcggca cgagttttac accatcacca aaaccagaa 120
ttttatgatg agattaaaat agagttgccc actcagctgc atgaaaagca ccacctgttg 180
ctcacattct tccatgtcag ctgtgacaac tcaagtaaag gaagcacgaa gaagagggat 240
gtcgttgaaa cccaagttgg ctactcctgg cttcccctcc tgaaagacgg aagggtgggtg 300
acaagcgagc agcacatccc ggtctcggcg aaccttcctt cgggctatct tggctaccaa 360
gagcttgagg tgggcaggca ttatgggtccg gaaattaaat gggtagatgg aggcaagcca 420
ctgctgaaaa tttccactca tctggtttct acagggatac tcaggatcag catttacata 480
attttttcca gtactgtcag aaaaccgaat ctggagccca agccttagga aacgaacttg 540
taaagtacct taagagtctg catgcg atg gaa ggc cac gtg atg atc gcc ttc 593
Met Glu Gly His Val Met Ile Ala Phe

1

5

ttg ccc act atc cta aac cag ctg ttc cga gtc ctc acc aga gcc aca 641
Leu Pro Thr Ile Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr
10 15 20 25

cag gaa gaa gtc gcg gtt aac gtg act cgg gtc att att cat gtg gtt 689
Gln Glu Glu Val Ala Val Asn Val Thr Arg Val Ile Ile His Val Val
30 35 40

gcc cag tgc cat gag gaa gga ttg gag agc cac ttg agg tca tat gtt 737
Ala Gln Cys His Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val
45 50 55

aag tac gcg tat aag gct gag cca tat gtt gcc tct gaa tac aag aca 785
Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr
60 65 70

gtg cat gaa gaa ctg acc aaa tcc atg acc acg att ctc aag cct tct 833
Val His Glu Glu Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser
75 80 85

gcc gat ttc ctc acc agc aac aaa cta ctg agg tac tca tgg ttt ttc 881

Q26
mt

Ala 90	Asp	Phe	Leu	Thr	Ser 95	Asn	Lys	Leu	Leu	Arg 100	Tyr	Ser	Trp	Phe	Phe 105	
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aaa Lys	ggt Val	aag Lys	ttg Leu 125	ctg Leu	cga Arg	aac Asn	cag Gln	aga Arg 130	ttt Phe	cct Pro	gca Ala	tcc Ser	tat Tyr	cat His	cat His	977
gca Ala	gcg Ala	gaa Glu 140	acc Thr	gtt Val	gta Val	aat Asn	atg Met 145	ctg Leu	atg Met	cca Pro	cac His	atc Ile	act Thr	cag Gln	aag Lys	1025
ttt Phe 155	gga Gly	gat Asp	aat Asn	cca Pro	gag Glu	gca Ala 160	tct Ser	aag Lys	aac Asn	gcg Ala 165	aat Asn	cat His	agc Ser	ctt Leu	gct Ala	1073
gtc Val 170	ttc Phe	atc Ile	aag Lys	aga Arg	tgt Cys 175	ttc Phe	acc Thr	ttc Phe	atg Met	gac Asp 180	agg Arg	ggc Gly	ttt Phe	gtc Val	ttc Phe 185	1121
aag Lys	cag Gln	atc Ile	aac Asn	aac Asn	tac Tyr	att Ile	agc Ser	tgt Cys	ttt Phe 195	gct Ala	cct Pro	gga Gly	gac Asp	cca Pro	aag Lys	1169
acc Thr	ctc Leu	ttt Phe	gaa Glu 205	tac Tyr	aag Lys	ttt Phe	gaa Glu	ttt Phe 210	ctc Leu	cgt Arg	gta Val	gtg Val	tgc Cys 215	aac Asn	cat His	1217
gaa Glu	cat His	tat Tyr 220	att Ile	ccg Pro	ttg Leu	aac Asn	tta Leu 225	cca Pro	atg Met	cca Pro	ttt Phe	gga Gly 230	aaa Lys	ggc Gly	agg Arg	1265
att Ile 235	caa Gln	aga Arg	tac Tyr	caa Gln	gac Asp	ctc Leu	cag Gln	ctt Leu	gac Asp	tac Tyr	tca Ser	tta Leu	aca Thr	gat Asp	gag Glu	1313
ttc Phe 250	tgc Cys	aga Arg	aac Asn	cac His	ttc Phe 255	ttg Leu	gtg Val	gga Gly	ctg Leu	tta Leu 260	ctg Leu	agg Arg	gag Glu	gtg Val	ggg Gly 265	1361
aca Thr	gcc Ala	ctc Leu	cag Gln	gag Glu	ttc Phe 270	cgg Arg	gag Glu	gtc Val	cgt Arg 275	ctg Leu	atc Ile	gcc Ala	atc Ile	agt Ser	gtg Val	1409

a26
only.

Ala	Asp	Phe	Leu	Thr	Ser	Asn	Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	
90					95					100					105	
ttt	gat	gta	ctg	atc	aaa	tct	atg	gct	cag	cat	ttg	ata	gag	aac	tcc	929
Phe	Asp	Val	Leu	Ile	Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	
				110					115					120		
aaa	gtt	aag	ttg	ctg	cga	aac	cag	aga	ttt	cct	gca	tcc	tat	cat	cat	977
Lys	Val	Lys	Leu	Leu	Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	
			125					130					135			
gca	gcg	gaa	acc	gtt	gta	aat	atg	ctg	atg	cca	cac	atc	act	cag	aag	1025
Ala	Ala	Glu	Thr	Val	Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	
		140					145					150				
ttt	gga	gat	aat	cca	gag	gca	tct	aag	aac	gcg	aat	cat	agc	ctt	gct	1073
Phe	Gly	Asp	Asn	Pro	Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	
	155					160					165					
gtc	ttc	atc	aag	aga	tgt	ttc	acc	ttc	atg	gac	agg	ggc	ttt	gtc	ttc	1121
Val	Phe	Ile	Lys	Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	
170					175					180					185	
aag	cag	atc	aac	aac	tac	att	agc	tgt	ttt	gct	cct	gga	gac	cca	aag	1169
Lys	Gln	Ile	Asn	Asn	Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	
				190					195					200		
acc	ctc	ttt	gaa	tac	aag	ttt	gaa	ttt	ctc	cgt	gta	gtg	tgc	aac	cat	1217
Thr	Leu	Phe	Glu	Tyr	Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	
			205					210					215			
gaa	cat	tat	att	ccg	ttg	aac	tta	cca	atg	cca	ttt	gga	aaa	ggc	agg	1265
Glu	His	Tyr	Ile	Pro	Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	
		220				225						230				
att	caa	aga	tac	caa	gac	ctc	cag	ctt	gac	tac	tca	tta	aca	gat	gag	1313
Ile	Gln	Arg	Tyr	Gln	Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	
	235					240				245						
ttc	tgc	aga	aac	cac	ttc	ttg	gtg	gga	ctg	tta	ctg	agg	gag	gtg	ggg	1361
Phe	Cys	Arg	Asn	His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	
250				255					260						265	
aca	gcc	ctc	cag	gag	ttc	cgg	gag	gtc	cgt	ctg	atc	gcc	atc	agt	gtg	1409
Thr	Ala	Leu	Gln	Glu	Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	
			270					275						280		
ctc	aag	aac	ctg	ctg	ata	aag	cat	tct	ttt	gat	gac	aga	tat	gct	tca	1457
Leu	Lys	Asn	Leu	Leu	Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	
			285					290					295			
agg	agc	cat	cag	gca	agg	ata	gcc	acc	ctc	tac	ctg	cct	ctg	ttt	ggt	1505
Arg	Ser	His	Gln	Ala	Arg	Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	
		300				305						310				
ctg	ctg	att	gaa	aac	gtc	cag	cgg	atc	aat	gtg	agg	gat	gtg	tca	ccc	1553
Leu	Leu	Ile	Glu	Asn	Val	Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	
		315				320					325					
ttc	cct	gtg	aac	gcg	ggc	atg	acc	gtg	aag	gat	gaa	tcc	ctg	gct	cta	1601
Phe	Pro	Val	Asn	Ala	Gly	Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	

926
cont.

330	335	340	345	
cca gct gtg aat ccg ctg gtg acg ccg cag aag gga agc acc ctg gac Pro Ala Val Asn Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp	350	355	360	1649
aac agc ctg cac aag gac ctg ctg ggc gcc atc tcc ggc att gct tct Asn Ser Leu His Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser	365	370	375	1697
cca tat aca acc tca act cca aac atc aac agt gtg aga aat gct gat Pro Tyr Thr Thr Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp	380	385	390	1745
tcg aga gga tct ctc ata agc aca gat tcg ggt aac agc ctt cca gaa Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu	395	400	405	1793
agg aat agt gag aag agc aat tcc ctg gat aag cac caa caa agt agc Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser	410	415	420	1841
aca ttg gga aat tcc gtg gtt cgc tgt gat aaa ctt gac cag tct gag Thr Leu Gly Asn Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu	430	435	440	1889
att aag agc cta ctg atg tgt ttc ctc tac atc tta aag agc atg tct Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser	445	450	455	1937
gat gat gct ttg ttt aca tat tgg aac aag gct tca aca tct gaa ctt Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu	460	465	470	1985
atg gat ttt ttt aca ata tct gaa gtc tgc ctg cac cag ttc cag tac Met Asp Phe Phe Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr	475	480	485	2033
atg ggg aag cga tac ata gcc agg aac cag gag ggg ttg gga ccc ata Met Gly Lys Arg Tyr Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile	490	495	500	2081
gtt cat gat cga aag tct cag aca ttg cct gtt tcc cgt aac aga aca Val His Asp Arg Lys Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr	510	515	520	2129
gga atg atg cat gcc aga ttg cag cag ctg ggc agc ctg gat aac tct Gly Met Met His Ala Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser	525	530	535	2177
ctc act ttt aac cac agc tat ggc cac tcg gac gca gat gtt ctg cac Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp Ala Asp Val Leu His	540	545	550	2225
cag tca tta ctt gaa gcc aac att gct act gag gtt tgc ctg aca gct Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala	555	560	565	2273
ctg gac acg ctt tct cta ttt aca ttg gcg ttt aag aac cag ctc ctg Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu	570	575	580	2321
			585	

a26
ent.

gcc gac cat gga cat aat cct ctc atg aaa aaa gtt ttt gat gtc tac	2369
Ala Asp His Gly His Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr	
590 595 600	
ctg tgt ttt ctt caa aaa cat cag tct gaa acg gct tta aaa aat gtc	2417
Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val	
605 610 615	
ttc act gcc tta agg tcc tta att tat aag ttt ccc tca aca ttc tat	2465
Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr	
620 625 630	
gaa ggg aga gcg gac atg tgt gcg gct ctg tgt tac gag att ctc aag	2513
Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys	
635 640 645	
tgc tgt aac tcc aag ctg agc tcc atc agg acg gag gcc tcc cag ctg	2561
Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu	
650 655 660 665	
ctc tac ttc ctg atg agg aac aac ttt gat tac act gga aag aag tcc	2609
Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser	
670 675 680	
ttt gtc cgg aca cat ttg caa gtc atc ata tct gtc agc cag ctg ata	2657
Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile	
685 690 695	
gca gac gtt gtt ggc att ggg gaa acc aga ttc cag cag tcc ctg tcc	2705
Ala Asp Val Val Gly Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser	
700 705 710	
atc atc aac aac tgt gcc aac agt gac cgg ctt att aag cac acc agc	2753
Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser	
715 720 725	
ttc tcc tct gat gtg aag gac tta acc aaa agg ata cgc acg gtg cta	2801
Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu	
730 735 740 745	
atg gcc acc gcc cag atg aag gag cat gag aac gac cca gag atg ctg	2849
Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met Leu	
750 755 760	
gtg gac ctc cag tac agc ctg gcc aaa tcc tat gcc agc acg ccc gag	2897
Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu	
765 770 775	
ctc agg aag acg tgg ctc gac agc atg gcc agg atc cat gtc aaa aat	2945
Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys Asn	
780 785 790	
ggc gat ctc tca gag gca gca atg tgc tat gtc cac gta aca gcc cta	2993
Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val His Val Thr Ala Leu	
795 800 805	
gtg gca gaa tat ctc aca cgg aaa ggc gtg ttt aga caa gga tgc acc	3041
Val Ala Glu Tyr Leu Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr	
810 815 820 825	

q26
cont.

gcc ttc agg gtc att acc cca aac atc gac gag gag gcc tcc atg atg 3089
 Ala Phe Arg Val Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met
 830 835 840

gaa gac gtg ggg atg cag gat gtc cat ttc aac gag gat gtg ctg atg 3137
 Glu Asp Val Gly Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met
 845 850 855

gag ctc ctt gag cag tgc gca gat gga ctc tgg aaa gcc gag cgc tac 3185
 Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr
 860 865 870

gag ctc atc gcc gac atc tac aaa ctt atc atc ccc att tat gag aag 3233
 Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys
 875 880 885

cgg agg gat ttc ttt gaa gat gaa gat gga aag gag tat att tac aag 3281
 Arg Arg Asp Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys
 890 895 900 905

gaa ccc aaa ctc aca ccg ctg tcg gaa att tct cag aga ctc ctt aaa 3329
 Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys
 910 915 920

ctg tac tcg gat aaa ttt ggt tct gaa aat gtc aaa atg ata cag gat 3377
 Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp
 925 930 935

tct ggc aag gtc aac cct aag gat ctg gat tct aag tat gca tac atc 3425
 Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile
 940 945 950

cag gtg act cac gtc atc ccc ttc ttt gac gaa aaa gag ttg caa gaa 3473
 Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu
 955 960 965

agg aaa aca gag ttt gag aga tcc cac aac atc cgc cgc ttc atg ttt 3521
 Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe
 970 975 980 985

gag atg cca ttt acg cag acc ggg aag agg cag ggc ggg gtg gaa gag 3569
 Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu
 990 995 1000

cag tgc aaa cgg cgc acc atc ctg aca gcc ata cac tgc ttc cct tat 3617
 Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr
 1005 1010 1015

gtg aag aag cgc atc cct gtc atg tac cag cac cac act gac ctg aac 3665
 Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn
 1020 1025 1030

ccc atc gag gtg gcc att gac gag atg agt aag aag gtg gcg gag ctc 3713
 Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu
 1035 1040 1045

cgg cag ctg tgc tcc tcg gcc gag gtg gac atg atc aaa ctg cag ctc 3761
 Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu
 1050 1055 1060 1065

aaa ctc cag ggc agc gtg agt gtt cag gtc aat gct ggc cca cta gca 3809

Lys	Leu	Gln	Gly	Ser	Val	Ser	Val	Gln	Val	Asn	Ala	Gly	Pro	Leu	Ala		
				1070					1075					1080			
tat	gcg	cga	gct	ttc	tta	gat	gat	aca	aac	aca	aag	cga	tat	cct	gac	3857	
Tyr	Ala	Arg	Ala	Phe	Leu	Asp	Asp	Thr	Asn	Thr	Lys	Arg	Tyr	Pro	Asp		
			1085					1090					1095				
aat	aaa	gtg	aag	ctg	ctt	aag	gaa	gtt	ttc	agg	caa	ttt	gtg	gaa	gct	3905	
Asn	Lys	Val	Lys	Leu	Leu	Lys	Glu	Val	Phe	Arg	Gln	Phe	Val	Glu	Ala		
		1100					1105					1110					
tgc	ggt	caa	gcc	tta	gcg	gta	aac	gaa	cgt	ctg	att	aaa	gaa	gac	cag	3953	
Cys	Gly	Gln	Ala	Leu	Ala	Val	Asn	Glu	Arg	Leu	Ile	Lys	Glu	Asp	Gln		
	1115				1120					1125							
ctc	gag	tat	cag	gaa	gaa	atg	aaa	gcc	aac	tac	agg	gaa	atg	gcg	aag	4001	
Leu	Glu	Tyr	Gln	Glu	Glu	Met	Lys	Ala	Asn	Tyr	Arg	Glu	Met	Ala	Lys		
1130				1135					1140				1145				
gag	ctt	tct	gaa	atc	atg	cat	gag	cag	atc	tgc	ccc	ctg	gag	gag	aag	4049	
Glu	Leu	Ser	Glu	Ile	Met	His	Glu	Gln	Ile	Cys	Pro	Leu	Glu	Glu	Lys		
			1150					1155				1160					
acg	agc	gtc	tta	ccg	aat	tcc	ctt	cac	atc	ttc	aac	gcc	atc	agt	ggg	4097	
Thr	Ser	Val	Leu	Pro	Asn	Ser	Leu	His	Ile	Phe	Asn	Ala	Ile	Ser	Gly		
		1165					1170					1175					
act	cca	aca	agc	aca	atg	gtt	cac	ggg	atg	acc	agc	tcg	tct	tcg	gtc	4145	
Thr	Pro	Thr	Ser	Thr	Met	Val	His	Gly	Met	Thr	Ser	Ser	Ser	Ser	Val		
	1180					1185					1190						
gtg	tgattacatc	tcattggccc	gtgtgtgggga	cttgctttgt	catttgcaaa											4198	
Val																	
ctcaggatgc	tttccaaagc	caatcactgg	ggagaccgag	cacagggagg	accaagggga											4258	
aggggagaga	aaggaaataa	agaacaacgt	tattttcttaa	cagactttct	ataggagtgtg											4318	
taagaagggtg	cacatatttt	tttaaattctc	actggcaata	ttcaaagttt	tcattgtgtc											4378	
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tagtgttaga	atagatggcc	tacagaaaaa	aaaggttctg	ggatctacat	ggcagggagg											4498	
gctgcactga	cattgatgcc	tgggggacct	tttgcctcga	ctcgtgccgg	aaatctgatc											4558	
gtaatcaggg	tacagaactt	actagttttg	tctaggagta	tgttgtatga	ctaggatttg											4618	
tgctattatc	tcattcaaca	acatagagca	agaatagtga	gctaactgag	ctagacactc											4678	
aattaatccg	ctactggctt	caagtcagaa	ctttgtcatt	aatcatcgac	tccgggacgg											4738	
tcatatatgt	attacatttc	tacattttta	atactcacat	gggcttatgc	attaagttta											4798	
attgtgataa	atttgtgctg	gtccagtata	tgcaatacac	tttaatgggt	tattcttgtc											4858	
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<212> PRT
 <213> Homo sapiens
 <223> Human CLASP-2

<400> 88

Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln
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Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn
 20 25 30

Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly
 35 40 45

Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu
 50 55 60

Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys
 65 70 75 80

Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn
 85 90 95

Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys Ser
 100 105 110

Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg Asn
 115 120 125

Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val Asn
 130 135 140

Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu Ala
 145 150 155 160

Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys Phe
 165 170 175

Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile
 180 185 190

Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe
 195 200 205

Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn
 210 215 220

Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu
 225 230 235 240

Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu
 245 250 255

Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg
 260 265 270

Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys
 275 280 285

His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile
 290 295 300

926
 cont.

Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	Val	Gln	305	310	315	320
Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	Gly	Met	325	330	335	
Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	Leu	Val	340	345	350	
Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp	Leu	355	360	365	
Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	Thr	Pro	370	375	380	
Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Ser	385	390	395	400
Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys	Ser	Asn	405	410	415	
Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser	Val	Val	420	425	430	
Arg	Cys	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met	Cys	435	440	445	
Phe	Leu	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	Tyr	450	455	460	
Trp	Asn	Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	Thr	Ile	Ser	465	470	475	480
Glu	Val	Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg	Tyr	Ile	Ala	485	490	495	
Arg	Asn	Gln	Glu	Gly	Leu	Gly	Pro	Ile	Val	His	Asp	Arg	Lys	Ser	Gln	500	505	510	
Thr	Leu	Pro	Val	Ser	Arg	Asn	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	515	520	525	
Gln	Gln	Leu	Gly	Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser	Tyr	530	535	540	
Gly	His	Ser	Asp	Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	545	550	555	560
Ile	Ala	Thr	Glu	Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu	Phe	565	570	575	
Thr	Leu	Ala	Phe	Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	580	585	590	
Leu	Met	Lys	Lys	Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His	595	600	605	
Gln	Ser	Glu	Thr	Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser	Leu	610	615	620	

Q26
cont.

Ile	Tyr	Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	625	630	635	640
Ala	Ala	Leu	Cys	Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	645	650	655	
Ser	Ile	Arg	Thr	Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	660	665	670	
Asn	Phe	Asp	Tyr	Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	675	680	685	
Val	Ile	Ile	Ser	Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Val	Gly	Ile	Gly	690	695	700	
Glu	Thr	Arg	Phe	Gln	Gln	Ser	Leu	Ser	Ile	Ile	Asn	Asn	Cys	Ala	Asn	705	710	715	720
Ser	Asp	Arg	Leu	Ile	Lys	His	Thr	Ser	Phe	Ser	Ser	Asp	Val	Lys	Asp	725	730	735	
Leu	Thr	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	740	745	750	
Glu	His	Glu	Asn	Asp	Pro	Glu	Met	Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	755	760	765	
Ala	Lys	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	770	775	780	
Ser	Met	Ala	Arg	Ile	His	Val	Lys	Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	785	790	795	800
Met	Cys	Tyr	Val	His	Val	Thr	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	805	810	815	
Lys	Gly	Val	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile	Thr	Pro	820	825	830	
Asn	Ile	Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Met	Gln	Asp	835	840	845	
Val	His	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln	Cys	Ala	850	855	860	
Asp	Gly	Leu	Trp	Lys	Ala	Glu	Arg	Tyr	Glu	Leu	Ile	Ala	Asp	Ile	Tyr	865	870	875	880
Lys	Leu	Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe	Phe	Glu	Asp	885	890	895	
Glu	Asp	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	900	905	910	
Ser	Glu	Ile	Ser	Gln	Arg	Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	915	920	925	
Ser	Glu	Asn	Val	Lys	Met	Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	930	935	940	
Asp	Leu	Asp	Ser	Lys	Tyr	Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Ile	Pro				

Q26
cont.

945		950		955		960
Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg						
		965		970		975
Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr						
		980		985		990
Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile						
		995		1000		1005
Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val						
		1010		1015		1020
Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp						
		1025		1030		1035
						1040
Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala						
		1045		1050		1055
Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser						
		1060		1065		1070
Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp						
		1075		1080		1085
Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys						
		1090		1095		1100
Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val						
		1105		1110		1115
						1120
Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met						
		1125		1130		1135
Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His						
		1140		1145		1150
Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser						
		1155		1160		1165
Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val						
		1170		1175		1180
His Gly Met Thr Ser Ser Ser Ser Val Val						
		1185		1190		

<210> 89

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Furin cleavage
consensus sequence

<400> 89

Arg Lys Gln Arg

1

<210> 90
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Human CLASP-2
predicted cleavage site by homology

<400> 90
Arg Asn Gln Arg
1

<210> 91
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved
consensus motif E

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = any amino acid

076
cont.
<220>
<221> MOD_RES
<222> (6)
<223> Xaa = any amino acid

<400> 91
Pro Glu Xaa Ala Ile Xaa Met
1 5

<210> 92
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved
consensus motif F

<220>
<221> MOD_RES
<222> (1)..(15)
<223> Xaa is any amino acid.

<400> 92
Leu Xaa Met Xaa Leu Gly Xaa Val Xaa Xaa Xaa Val Asn Xaa Gly
1 5 10 15

<210> 93
<211> 125

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP-2C exon
not found in CLASP-2A

<220>

<221> misc_feature

<222> (1)..(125)

<223> N is A, C, G, or T.

<400> 93

agggattttg agaggctggc ccattctgtat gacacgctgc accgggccta cagcaaagtg 60
accgaggtca tgcactcggg ccgcagttnc tggggaccta cttccgggta gccttcttcg 120
ggcag 125

<210> 94

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acids
encoded by CLASP-2C exon not found in CLASP-2A

<400> 94

Arg Asp Phe Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala
1 5 10 15

Tyr Ser Lys Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly
20 25 30

Thr Tyr Phe Arg Val Ala Phe Phe Gly Gln Gly Phe
35 40

<210> 95

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Exemplary
probe/primer F1

<400> 95

cccagatttt tatgatgag

19

<210> 96

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Exemplary
probe/primer R1

<400> 96

gataatgaca aagttctgac

20

<210> 97

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Exemplary
probe/primer F2

<400> 97

ctggaaatct tgacaaaaat gc

22

<210> 98

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Exemplary
probe/primer R2

<400> 98

gtcttttttaa tacagatgtg g

21

<210> 99

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Exemplary
probe/primer F3

<400> 99

gagaggctgg cccatctgta tg

22

<210> 100

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Exemplary
probe/primer R3

<400> 100

atcttcaaag aatccctgcc

20

<210> 101

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

926
unt.

<223> Description of Artificial Sequence: Exemplary
probe/primer F4

<400> 101
gaagcagtcc agtgggagcc g

21

<210> 102
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer R4

<400> 102
gcctccccgg ctctctctca gg

22

<210> 103
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer R5

<400> 103
cctccacatc tgtttcactg tc

22

<210> 104
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer F5

<400> 104
ctccatgatg gaagacgtgg g

21

<210> 105
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer R6

<400> 105
gatgagctcg tagcgctcgg c

21

<210> 106
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer F6

<400> 106
cattggcggtt taagctcctg

20

<210> 107
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer F7

<400> 107
ggacccatag ttcgatgcg

20

<210> 108
<211> 22
<212> DNA
<213> Artificial Sequence

Q26
cont.
<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer R4

<400> 108
cttcattcttc aagaaatccc tc

22

<210> 109
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
oligo 1

<400> 109
gaaggcgatc atcacgtggc cttccatcgc

30

<210> 110
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
oligo 2

<400> 110
gcttcaagta atgactgggtg cagaacatct g

31

<210> 111
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
oligo 3

<400> 111
gctcctcctc aggcaggcgc tatggctgtg g 31

<210> 112
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
oligo 4

<400> 112
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Q26
cont.
<210> 113
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
oligo 5

<400> 113
gcaatgtctg agactttcga tcatgaacta tg 32

<210> 114
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
oligo 6

<400> 114
caggagctgg ttcttaaa 18

<210> 115
<211> 81
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 1A

<400> 115
gcaggggaaa aacctggccc catgattcac ttacttccca cggatctct cccatgacac 60
gtgaggatta ttacaattta a 81

<210> 116
<211> 118
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 1B

<400> 116
ttatcccttt actacttgcg aagtgagttc ggtagatggg agtggagaag agaaccttag 60
aatcattgtt tagtcttcat ctttcacagc tcaggctgaa ggcctttcct tgctgaga 118

<210> 117
<211> 42
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 1C

<400> 117
gcggcagagc gtgtctgagg tgggtgcgcgg ctccgtgctc ct 42

<210> 118
<211> 6791
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (102) .. (6044)

<220>
<223> Human CLASP-2 gene

<400> 118
ggcaaagcca aagctaattg agcaagctaa ttgagccact cgactatgaa aatgtcatcg 60
tccagaagaa gactcagatc ctgaacgact gtttacggga g atg ctg ctc ttc cct 116
Met Leu Leu Phe Pro
1 5

tac gat gac ttt cag acg gcc atc ctg aga cga cag ggt cga tac ata 164
Tyr Asp Asp Phe Gln Thr Ala Ile Leu Arg Arg Gln Gly Arg Tyr Ile
10 15 20

tgc tca aca gtg cct gcg aag gcg gaa gag gaa gca cag agc ttg ttt 212
Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Glu Ala Gln Ser Leu Phe
25 30 35

gtt aca gag tgc atc aaa acc tat aac tct gac tgg cat ctt gtg aac 260
Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp Trp His Leu Val Asn
40 45 50

tat	aaa	tat	gaa	gat	tac	tca	gga	gag	ttt	cga	cag	ctt	ccg	aac	aaa	308
Tyr	Lys	Tyr	Glu	Asp	Tyr	Ser	Gly	Glu	Phe	Arg	Gln	Leu	Pro	Asn	Lys	
	55					60					65					
gtg	gtc	aag	ttg	gat	aaa	ctt	cca	gtt	cat	gtc	tat	gaa	gtt	gac	gag	356
Val	Val	Lys	Leu	Asp	Lys	Leu	Pro	Val	His	Val	Tyr	Glu	Val	Asp	Glu	
	70				75				80						85	
gag	gtc	gac	aaa	gat	gag	gat	gct	gcc	tcc	ctt	ggg	tcc	cag	aag	ggg	404
Glu	Val	Asp	Lys	Asp	Glu	Asp	Ala	Ala	Ser	Leu	Gly	Ser	Gln	Lys	Gly	
				90					95					100		
ggg	atc	acc	aag	cat	ggc	tgg	ctg	tac	aaa	ggc	aac	atg	aac	agt	gcc	452
Gly	Ile	Thr	Lys	His	Gly	Trp	Leu	Tyr	Lys	Gly	Asn	Met	Asn	Ser	Ala	
			105					110					115			
atc	agc	gtg	acc	atg	agg	tca	ttt	aag	aga	cga	ttt	ttc	cac	ctg	att	500
Ile	Ser	Val	Thr	Met	Arg	Ser	Phe	Lys	Arg	Arg	Phe	Phe	His	Leu	Ile	
		120					125					130				
caa	ctt	ggc	gat	gga	tcc	tat	aat	ttg	aat	ttt	tat	aaa	gat	gaa	aag	548
Gln	Leu	Gly	Asp	Gly	Ser	Tyr	Asn	Leu	Asn	Phe	Tyr	Lys	Asp	Glu	Lys	
	135					140					145					
atc	tcc	aaa	gaa	cca	aaa	gga	tca	ata	ttt	ctg	gat	tcc	tgt	atg	ggg	596
Ile	Ser	Lys	Glu	Pro	Lys	Gly	Ser	Ile	Phe	Leu	Asp	Ser	Cys	Met	Gly	
	150				155					160					165	
gtc	gtt	cag	aac	aac	aaa	gtc	agg	cgt	ttt	gct	ttt	gag	ctc	aag	atg	644
Val	Val	Gln	Asn	Asn	Lys	Val	Arg	Arg	Phe	Ala	Phe	Glu	Leu	Lys	Met	
				170					175					180		
cag	gac	aaa	agt	agt	tat	ctc	ttg	gca	gca	gac	agt	gaa	gtg	gaa	atg	692
Gln	Asp	Lys	Ser	Ser	Tyr	Leu	Leu	Ala	Ala	Asp	Ser	Glu	Val	Glu	Met	
			185					190					195			
gaa	gaa	tgg	atc	aca	att	cta	aat	aag	atc	ctc	cag	ctc	aac	ttt	gaa	740
Glu	Glu	Trp	Ile	Thr	Ile	Leu	Asn	Lys	Ile	Leu	Gln	Leu	Asn	Phe	Glu	
		200					205					210				
gct	gca	atg	caa	gaa	aag	cga	aat	ggc	gac	tct	cac	gaa	gat	gat	gaa	788
Ala	Ala	Met	Gln	Glu	Lys	Arg	Asn	Gly	Asp	Ser	His	Glu	Asp	Asp	Glu	
	215					220					225					
caa	agc	aaa	ttg	gaa	ggg	tct	ggg	tcc	ggg	tta	gat	agc	tac	ctg	ccg	836
Gln	Ser	Lys	Leu	Glu	Gly	Ser	Gly	Ser	Gly	Leu	Asp	Ser	Tyr	Leu	Pro	
	230				235					240					245	
gaa	ctt	gcc	aag	agt	gca	aga	gaa	gca	gaa	atc	aaa	cta	aaa	agt	gaa	884
Glu	Leu	Ala	Lys	Ser	Ala	Arg	Glu	Ala	Glu	Ile	Lys	Leu	Lys	Ser	Glu	
				250				255						260		
agc	aga	gtc	aaa	ctt	ttt	tat	ttg	gac	cca	gat	gcc	cag	aag	ctt	gac	932
Ser	Arg	Val	Lys	Leu	Phe	Tyr	Leu	Asp	Pro	Asp	Ala	Gln	Lys	Leu	Asp	
			265					270					275			
ttc	tca	tca	gct	gag	cca	gaa	gtg	aag	tca	ttt	gaa	gag	aag	ttt	gga	980
Phe	Ser	Ser	Ala	Glu	Pro	Glu	Val	Lys	Ser	Phe	Glu	Glu	Lys	Phe	Gly	
		280					285					290				

026
cont.

aaa	agg	atc	ctt	gtc	aag	tgc	aat	gat	tta	tct	ttc	aat	ttg	caa	tgc	1028
Lys	Arg	Ile	Leu	Val	Lys	Cys	Asn	Asp	Leu	Ser	Phe	Asn	Leu	Gln	Cys	
	295					300					305					
tgt	gtt	gcc	gaa	aat	gaa	gaa	gga	ccc	act	aca	aat	gtt	gaa	cct	ttc	1076
Cys	Val	Ala	Glu	Asn	Glu	Glu	Gly	Pro	Thr	Thr	Asn	Val	Glu	Pro	Phe	
310					315					320					325	
ttt	gtt	act	cta	tcc	ctg	ttt	gac	ata	aaa	tac	aac	cgg	aag	att	tct	1124
Phe	Val	Thr	Leu	Ser	Leu	Phe	Asp	Ile	Lys	Tyr	Asn	Arg	Lys	Ile	Ser	
				330					335					340		
gcc	gat	ttc	cac	gta	gac	ctg	aac	cat	ttc	tca	gtg	agg	caa	atg	ctc	1172
Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Phe	Ser	Val	Arg	Gln	Met	Leu	
			345					350					355			
gcc	acc	acg	tcc	ccg	gcg	ctg	atg	aat	ggc	agt	ggg	cag	agc	cca	tct	1220
Ala	Thr	Thr	Ser	Pro	Ala	Leu	Met	Asn	Gly	Ser	Gly	Gln	Ser	Pro	Ser	
		360					365					370				
gtc	ctc	aag	ggc	atc	ctt	cat	gaa	gcc	gcc	atg	cag	tat	ccg	aag	cag	1268
Val	Leu	Lys	Gly	Ile	Leu	His	Glu	Ala	Ala	Met	Gln	Tyr	Pro	Lys	Gln	
	375					380					385					
gga	ata	ttt	tca	gtc	act	tgt	cct	cat	cca	gat	ata	ttt	ctt	gtg	gcc	1316
Gly	Ile	Phe	Ser	Val	Thr	Cys	Pro	His	Pro	Asp	Ile	Phe	Leu	Val	Ala	
390					395					400					405	
aga	att	gaa	aaa	gtc	ctt	cag	ggg	agc	atc	aca	cat	tgc	gct	gag	cca	1364
Arg	Ile	Glu	Lys	Val	Leu	Gln	Gly	Ser	Ile	Thr	His	Cys	Ala	Glu	Pro	
				410					415					420		
tat	atg	aaa	agt	tca	gac	tct	tct	aag	gtg	gcc	cag	aag	gtg	ctg	aag	1412
Tyr	Met	Lys	Ser	Ser	Asp	Ser	Ser	Lys	Val	Ala	Gln	Lys	Val	Leu	Lys	
			425					430					435			
aat	gcc	aag	cag	gca	tgc	caa	aga	cta	gga	cag	tat	aga	atg	cca	ttt	1460
Asn	Ala	Lys	Gln	Ala	Cys	Gln	Arg	Leu	Gly	Gln	Tyr	Arg	Met	Pro	Phe	
		440					445					450				
gct	tgg	gca	gca	agg	aca	ttg	ttt	aag	gat	gca	tct	gga	aat	ctt	gac	1508
Ala	Trp	Ala	Ala	Arg	Thr	Leu	Phe	Lys	Asp	Ala	Ser	Gly	Asn	Leu	Asp	
	455					460					465					
aaa	aat	gcc	aga	ttt	tct	gcc	atc	tac	agg	caa	gac	agc	aat	aag	cta	1556
Lys	Asn	Ala	Arg	Phe	Ser	Ala	Ile	Tyr	Arg	Gln	Asp	Ser	Asn	Lys	Leu	
470					475					480					485	
tcc	aat	gat	gac	atg	ctc	aag	tta	ctt	gca	gac	ttt	cgg	aaa	cct	gag	1604
Ser	Asn	Asp	Asp	Met	Leu	Lys	Leu	Leu	Ala	Asp	Phe	Arg	Lys	Pro	Glu	
				490					495					500		
aag	atg	gct	aag	ctc	cca	gtg	att	tta	ggc	aat	cta	gac	att	aca	att	1652
Lys	Met	Ala	Lys	Leu	Pro	Val	Ile	Leu	Gly	Asn	Leu	Asp	Ile	Thr	Ile	
			505					510					515			
gat	aat	gtt	tcc	tca	gac	ttc	cct	aat	tat	gtt	aat	tca	tca	tac	att	1700
Asp	Asn	Val	Ser	Ser	Asp	Phe	Pro	Asn	Tyr	Val	Asn	Ser	Ser	Tyr	Ile	
		520					525					530				
ccc	aca	aaa	caa	ttt	gaa	acc	tgc	agt	aaa	act	ccc	atc	acg	ttt	gaa	1748

026
ent.

Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys	Thr	Pro	Ile	Thr	Phe	Glu		
535						540					545						
gtg	gag	gaa	ttt	gtg	ccc	tgc	ata	cca	aaa	cac	act	cag	cct	tac	acc	1796	
Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys	His	Thr	Gln	Pro	Tyr	Thr		
550					555					560					565		
atc	tac	acc	aat	cac	ctt	tac	gtt	tat	cct	aag	tac	ttg	aaa	tac	gac	1844	
Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro	Lys	Tyr	Leu	Lys	Tyr	Asp		
				570					575					580			
agt	cag	aag	tct	ttt	gcc	aag	gct	aga	aat	att	gcg	att	tgc	att	gaa	1892	
Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn	Ile	Ala	Ile	Cys	Ile	Glu		
			585					590					595				
ttc	aaa	gat	tca	gat	gag	gaa	gac	tct	cag	ccc	ctt	aag	tgc	att	tat	1940	
Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln	Pro	Leu	Lys	Cys	Ile	Tyr		
		600					605					610					
ggc	aga	cct	ggg	ggg	cca	gtt	ttc	aca	aga	agc	gcc	ttt	gct	gca	gtt	1988	
Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg	Ser	Ala	Phe	Ala	Ala	Val		
	615					620					625						
tta	cac	cat	cac	caa	aac	cca	gaa	ttt	tat	gat	gag	att	aaa	ata	gag	2036	
Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	Asp	Glu	Ile	Lys	Ile	Glu		
630					635					640					645		
ttg	ccc	act	cag	ctg	cat	gaa	aag	cac	cac	ctg	ttg	ctc	aca	ttc	ttc	2084	
Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	Leu	Leu	Leu	Thr	Phe	Phe		
				650					655					660			
cat	gtc	agc	tgt	gac	aac	tca	agt	aaa	gga	agc	acg	aag	aag	agg	gat	2132	
His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser	Thr	Lys	Lys	Arg	Asp		
			665					670					675				
gtc	gtt	gaa	acc	caa	gtt	ggc	tac	tcc	tgg	ctt	ccc	ctc	ctg	aaa	gac	2180	
Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu	Pro	Leu	Leu	Lys	Asp		
		680					685					690					
gga	agg	gtg	gtg	aca	agc	gag	cag	cac	atc	ccg	gtc	tcg	gcg	tac	ctt	2228	
Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	Pro	Val	Ser	Ala	Tyr	Leu		
	695					700					705						
cct	tcg	ggc	cat	ctt	ggc	tac	caa	gag	ctt	ggg	atg	ggc	agg	cat	tat	2276	
Pro	Ser	Gly	His	Leu	Gly	Tyr	Gln	Glu	Leu	Gly	Met	Gly	Arg	His	Tyr		
710					715					720					725		
ggg	ccg	gaa	att	aaa	tgg	gta	gat	gga	ggc	aag	cca	ctg	ctg	aaa	att	2324	
Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys	Pro	Leu	Leu	Lys	Ile		
				730					735					740			
tcc	act	cat	ctg	gtt	tct	aca	gtg	tat	act	cag	gat	cag	cat	tta	cat	2372	
Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln	Asp	Gln	His	Leu	His		
			745					750					755				
aat	ttt	ttc	cag	tac	tgt	cag	aaa	acc	gaa	tct	gga	gcc	caa	gcc	tta	2420	
Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser	Gly	Ala	Gln	Ala	Leu		
		760					765					770					
gga	aac	gaa	ctt	gta	aag	tac	ctt	aag	agt	ctg	cat	gcg	atg	gaa	ggc	2468	
Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu	His	Ala	Met	Glu	Gly		

Q26
cont.

775	780	785	
cac gtg atg atc gcc ttc ttg ccc act atc cta aac cag ctg ttc cga His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe Arg 790 795 800 805			2516
gtc ctc acc aga gcc aca cag gaa gaa gtc gcg gtt aac gtg act cgg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr Arg 810 815 820			2564
gtc att att cat gtg gtt gcc cag tgc cat gag gaa gga ttg gag agc Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu Ser 825 830 835			2612
cac ttg agg tca tat gtt aag tac gcg tat aag gct gag cca tat gtt His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr Val 840 845 850			2660
gcc tct gaa tac aag aca gtg cat gaa gaa ctg acc aaa tcc atg acc Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met Thr 855 860 865			2708
acg att ctc aag cct tct gcc gat ttc ctc acc agc aac aaa cta ctg Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu Leu 870 875 880 885			2756
agg tac tca tgg ttt ttc ttt gat gta ctg atc aaa tct atg gct cag Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys Ser Met Ala Gln 890 895 900			2804
cat ttg ata gag aac tcc aaa gtt aag ttg ctg cga aac cag aga ttt His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg Asn Gln Arg Phe 905 910 915			2852
cct gca tcc tat cat cat gca gcg gaa acc gtt gta aat atg ctg atg Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val Asn Met Leu Met 920 925 930			2900
cca cac atc act cag aag ttt gga gat aat cca gag gca tct aag aac Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu Ala Ser Lys Asn 935 940 945			2948
gcg aat cat agc ctt gct gtc ttc atc aag aga tgt ttc acc ttc atg Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys Phe Thr Phe Met 950 955 960 965			2996
gac agg ggc ttt gtc ttc aag cag atc aac aac tac att agc tgt ttt Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile Ser Cys Phe 970 975 980			3044
gct cct gga gac cca aag acc ctc ttt gaa tac aag ttt gaa ttt ctc Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe Glu Phe Leu 985 990 995			3092
cgt gta gtg tgc aac cat gaa cat tat att ccg ttg aac tta cca atg Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro Met 1000 1005 1010			3140
cca ttt gga aaa ggc agg att caa aga tac caa gac ctc cag ctt gac Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu Gln Leu Asp 1015 1020 1025			3188

026
cont

tac tca tta aca gat gag ttc tgc aga aac cac ttc ttg gtg gga ctg 3236
 Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu Val Gly Leu
 1030 1035 1040 1045
 tta ctg agg gag gtg ggg aca gcc ctc cag gag ttc cgg gag gtc cgt 3284
 Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg Glu Val Arg
 1050 1055 1060
 ctg atc gcc atc agt gtg ctc aag aac ctg ctg ata aag cat tct ttt 3332
 Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys His Ser Phe
 1065 1070 1075
 gat gac aga tat gct tca agg agc cat cag gca agg ata gcc acc ctc 3380
 Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile Ala Thr Leu
 1080 1085 1090
 tac ctg cct ctg ttt ggt ctg ctg att gaa aac gtc cag cgg atc aat 3428
 Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln Arg Ile Asn
 1095 1100 1105
 gtg agg gat gtg tca ccc ttc cct gtg aac gcg ggc atg acc gtg aag 3476
 Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met Thr Val Lys
 1110 1115 1120 1125
 gat gaa tcc ctg gct cta cca gct gtg aat ccg ctg gtg acg ccg cag 3524
 Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val Thr Pro Gln
 1130 1135 1140
 aag gga agc acc ctg gac aac agc ctg cac aag gac ctg ctg ggc gcc 3572
 Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu Leu Gly Ala
 1145 1150 1155
 atc tcc ggc att gct tct cca tat aca acc tca act cca aac atc aac 3620
 Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro Asn Ile Asn
 1160 1165 1170
 agt gtg aga aat gct gat tcg aga gga tct ctc ata agc aca gat tcg 3668
 Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser
 1175 1180 1185
 ggt aac agc ctt cca gaa agg aat agt gag aag agc aat tcc ctg gat 3716
 Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp
 1190 1195 1200 1205
 aag cac caa caa agt agc aca ttg gga aat tcc gtg gtt cgc tgt gat 3764
 Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp
 1210 1215 1220
 aaa ctt gac cag tct gag att aag agc cta ctg atg tgt ttc ctc tac 3812
 Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr
 1225 1230 1235
 atc tta aag agc atg tct gat gat gct ttg ttt aca tat tgg aac aag 3860
 Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys
 1240 1245 1250
 gct tca aca tct gaa ctt atg gat ttt ttt aca ata tct gaa gtc tgc 3908
 Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val Cys
 1255 1260 1265

026
ent.

ctg cac cag ttc cag tac atg ggg aag cga tac ata gcc agg aac cag Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala Arg Asn Gln 1270 1275 1280 1285	3956
gag ggg ttg gga ccc ata gtt cat gat cga aag tct cag aca ttg cct Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln Thr Leu Pro 1290 1295 1300	4004
gtt tcc cgt aac aga aca gga atg atg cat gcc aga ttg cag cag ctg Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu 1305 1310 1315	4052
ggc agc ctg gat aac tct ctc act ttt aac cac agc tat ggc cac tcg Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser 1320 1325 1330	4100
gac gca gat gtt ctg cac cag tca tta ctt gaa gcc aac att gct act Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr 1335 1340 1345	4148
gag gtt tgc ctg aca gct ctg gac acg ctt tct cta ttt aca ttg gcg Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala 1350 1355 1360 1365	4196
ttt aag aac cag ctc ctg gcc gac cat gga cat aat cct ctc atg aaa Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys 1370 1375 1380	4244
aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa cat cag tct gaa Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu 1385 1390 1395	4292
acg gct tta aaa aat gtc ttc act gcc tta agg tcc tta att tat aag Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys 1400 1405 1410	4340
ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg tgt gcg gct ctg Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu 1415 1420 1425	4388
tgt tac gag att ctc aag tgc tgt aac tcc aag ctg agc tcc atc agg Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg 1430 1435 1440 1445	4436
acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg aac aac ttt gat Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp 1450 1455 1460	4484
tac act gga aag aag tcc ttt gtc cgg aca cat ttg caa gtc atc ata Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile 1465 1470 1475	4532
tct gtc agc cag ctg ata gca gac gtt gtt ggc att ggg gaa acc aga Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu Thr Arg 1480 1485 1490	4580
ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc aac agt gac cgg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg 1495 1500 1505	4628
ctt att aag cac acc agc ttc tcc tct gat gtg aag gac tta acc aaa	4676

Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys	
1510	1515 1520 1525
agg ata cgc acg gtg cta atg gcc acc gcc cag atg aag gag cat gag	4724
Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu	
	1530 1535 1540
aac gac cca gag atg ctg gtg gac ctc cag tac agc ctg gcc aaa tcc	4772
Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser	
	1545 1550 1555
tat gcc agc acg ccc gag ctc agg aag acg tgg ctc gac agc atg gcc	4820
Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala	
	1560 1565 1570
agg atc cat gtc aaa aat ggc gat ctc tca gag gca gca atg tgc tat	4868
Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr	
	1575 1580 1585
gtc cac gta aca gcc cta gtg gca gaa tat ctc aca cgg aaa ggc gtg	4916
Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Gly Val	
	1590 1595 1600 1605
ttt aga caa gga tgc acc gcc ttc agg gtc att acc cca aac atc gac	4964
Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile Asp	
	1610 1615 1620
gag gag gcc tcc atg atg gaa gac gtg ggg atg cag gat gtc cat ttc	5012
Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His Phe	
	1625 1630 1635
aac gag gat gtg ctg atg gag ctc ctt gag cag tgc gca gat gga ctc	5060
Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu	
	1640 1645 1650
tgg aaa gcc gag cgc tac gag ctc atc gcc gac atc tac aaa ctt atc	5108
Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile	
	1655 1660 1665
atc ccc att tat gag aag cgg agg gat ttc ttt gaa gat gaa gat gga	5156
Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp Glu Asp Gly	
	1670 1675 1680 1685
aag gag tat att tac aag gaa ccc aaa ctc aca ccg ctg tcg gaa att	5204
Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile	
	1690 1695 1700
tct cag aga ctc ctt aaa ctg tac tcg gat aaa ttt ggt tct gaa aat	5252
Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn	
	1705 1710 1715
gtc aaa atg ata cag gat tct ggc aag gtc aac cct aag gat ctg gat	5300
Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp	
	1720 1725 1730
tct aag tat gca tac atc cag gtg act cac gtc atc ccc ttc ttt gac	5348
Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp	
	1735 1740 1745
gaa aaa gag ttg caa gaa agg aaa aca gag ttt gag aga tcc cac aac	5396
Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn	

Q26
cont.

1750	1755	1760	1765	
atc cgc cgc ttc atg ttt gag atg cca ttt acg cag acc ggg aag agg				5444
Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg				
	1770	1775	1780	
cag ggc ggg gtg gaa gag cag tgc aaa cgg cgc acc atc ctg aca gcc				5492
Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala				
	1785	1790	1795	
ata cac tgc ttc cct tat gtg aag aag cgc atc cct gtc atg tac cag				5540
Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln				
	1800	1805	1810	
cac cac act gac ctg aac ccc atc gag gtg gcc att gac gag atg agt				5588
His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser				
	1815	1820	1825	
aag aag gtg gcg gag ctc cgg cag ctg tgc tcc tcg gcc gag gtg gac				5636
Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp				
	1830	1835	1840	1845
atg atc aaa ctg cag ctc aaa ctc cag ggc agc gtg agt gtt cag gtc				5684
Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val				
	1850	1855	1860	
aat gct ggc cca cta gca tat gcg cga gct ttc tta gat gat aca aac				5732
Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn				
	1865	1870	1875	
aca aag cga tat cct gac aat aaa gtg aag ctg ctt aag gaa gtt ttc				5780
Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe				
	1880	1885	1890	
agg caa ttt gtg gaa gct tgc ggt caa gcc tta gcg gta aac gaa cgt				5828
Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg				
	1895	1900	1905	
ctg att aaa gaa gac cag ctc gag tat cag gaa gaa atg aaa gcc aac				5876
Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn				
	1910	1915	1920	1925
tac agg gaa atg gcg aag gag ctt tct gaa atc atg cat gag cag atc				5924
Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile				
	1930	1935	1940	
tgc ccc ctg gag gag aag acg agc gtc tta ccg aat tcc ctt cac atc				5972
Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile				
	1945	1950	1955	
ttc aac gcc atc agt ggg act cca aca agc aca atg gtt cac ggg atg				6020
Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly Met				
	1960	1965	1970	
acc agc tcg tct tcg gtc gtg tga ttacatctca tggcccgtgt gtggggactt				6074
Thr Ser Ser Ser Ser Val Val				
	1975	1980		
gctttgtcat ttgcaaactc aggatgcttt ccaaagccaa tcaactgggga gaccgagcac				6134
agggaggacc aaggggaagg ggagagaaag gaaataaaga acaacgttat ttcttaacag				6194

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ant.

actttctata ggagttgtaa gaaggtgcac atattttttt aaatctcact ggcaatattc 6254
aaagttttca ttgtgtctta acaaaggtgt ggtagacact.cttgagctgg acttagattt 6314
tattcttcct tgcagagtag tgtagaata gatggcctac agaaaaaaaaa ggttctggga 6374
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aatggtttat tcttgtcata aaaatgtgca atatggagat gtatacaagt ctttact 6791

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<211> 1980
<212> PRT
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<223> Human CLASP-2 gene

<400> 119
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Gln Gly Arg Tyr Ile Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Glu
20 25 30
Ala Gln Ser Leu Phe Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp
35 40 45
Trp His Leu Val Asn Tyr Lys Tyr Glu Asp Tyr Ser Gly Glu Phe Arg
50 55 60
Gln Leu Pro Asn Lys Val Val Lys Leu Asp Lys Leu Pro Val His Val
65 70 75 80
Tyr Glu Val Asp Glu Glu Val Asp Lys Asp Glu Asp Ala Ala Ser Leu
85 90 95
Gly Ser Gln Lys Gly Gly Ile Thr Lys His Gly Trp Leu Tyr Lys Gly
100 105 110
Asn Met Asn Ser Ala Ile Ser Val Thr Met Arg Ser Phe Lys Arg Arg
115 120 125
Phe Phe His Leu Ile Gln Leu Gly Asp Gly Ser Tyr Asn Leu Asn Phe
130 135 140
Tyr Lys Asp Glu Lys Ile Ser Lys Glu Pro Lys Gly Ser Ile Phe Leu
145 150 155 160
Asp Ser Cys Met Gly Val Val Gln Asn Asn Lys Val Arg Arg Phe Ala
165 170 175
Phe Glu Leu Lys Met Gln Asp Lys Ser Ser Tyr Leu Leu Ala Ala Asp
180 185 190
Ser Glu Val Glu Met Glu Glu Trp Ile Thr Ile Leu Asn Lys Ile Leu
195 200 205
Gln Leu Asn Phe Glu Ala Ala Met Gln Glu Lys Arg Asn Gly Asp Ser
210 215 220
His Glu Asp Asp Glu Gln Ser Lys Leu Glu Gly Ser Gly Ser Gly Leu
225 230 235 240
Asp Ser Tyr Leu Pro Glu Leu Ala Lys Ser Ala Arg Glu Ala Glu Ile
245 250 255

626
CNG.

Lys	Leu	Lys	Ser	Glu	Ser	Arg	Val	Lys	Leu	Phe	Tyr	Leu	Asp	Pro	Asp
			260					265					270		
Ala	Gln	Lys	Leu	Asp	Phe	Ser	Ser	Ala	Glu	Pro	Glu	Val	Lys	Ser	Phe
		275					280					285			
Glu	Glu	Lys	Phe	Gly	Lys	Arg	Ile	Leu	Val	Lys	Cys	Asn	Asp	Leu	Ser
	290					295					300				
Phe	Asn	Leu	Gln	Cys	Cys	Val	Ala	Glu	Asn	Glu	Glu	Gly	Pro	Thr	Thr
305					310					315					320
Asn	Val	Glu	Pro	Phe	Phe	Val	Thr	Leu	Ser	Leu	Phe	Asp	Ile	Lys	Tyr
				325					330					335	
Asn	Arg	Lys	Ile	Ser	Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Phe	Ser
			340				345						350		
Val	Arg	Gln	Met	Leu	Ala	Thr	Thr	Ser	Pro	Ala	Leu	Met	Asn	Gly	Ser
		355					360					365			
Gly	Gln	Ser	Pro	Ser	Val	Leu	Lys	Gly	Ile	Leu	His	Glu	Ala	Ala	Met
	370					375					380				
Gln	Tyr	Pro	Lys	Gln	Gly	Ile	Phe	Ser	Val	Thr	Cys	Pro	His	Pro	Asp
385					390					395					400
Ile	Phe	Leu	Val	Ala	Arg	Ile	Glu	Lys	Val	Leu	Gln	Gly	Ser	Ile	Thr
				405					410						415
His	Cys	Ala	Glu	Pro	Tyr	Met	Lys	Ser	Ser	Asp	Ser	Ser	Lys	Val	Ala
			420				425						430		
Gln	Lys	Val	Leu	Lys	Asn	Ala	Lys	Gln	Ala	Cys	Gln	Arg	Leu	Gly	Gln
		435					440					445			
Tyr	Arg	Met	Pro	Phe	Ala	Trp	Ala	Ala	Arg	Thr	Leu	Phe	Lys	Asp	Ala
	450					455					460				
Ser	Gly	Asn	Leu	Asp	Lys	Asn	Ala	Arg	Phe	Ser	Ala	Ile	Tyr	Arg	Gln
465					470					475					480
Asp	Ser	Asn	Lys	Leu	Ser	Asn	Asp	Asp	Met	Leu	Lys	Leu	Leu	Ala	Asp
				485					490					495	
Phe	Arg	Lys	Pro	Glu	Lys	Met	Ala	Lys	Leu	Pro	Val	Ile	Leu	Gly	Asn
			500					505					510		
Leu	Asp	Ile	Thr	Ile	Asp	Asn	Val	Ser	Ser	Asp	Phe	Pro	Asn	Tyr	Val
		515					520					525			
Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys	Thr
	530					535					540				
Pro	Ile	Thr	Phe	Glu	Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys	His
545					550					555					560
Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro	Lys
				565					570						575
Tyr	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn	Ile
			580				585						590		
Ala	Ile	Cys	Ile	Glu	Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln	Pro
		595					600					605			
Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg	Ser
	610					615					620				
Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	Asp
625					630					635					640
Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	Leu
				645					650					655	
Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser
			660				665						670		
Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu
		675					680					685			
Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	Pro
	690					695					700				
Val	Ser	Ala	Tyr	Leu	Pro	Ser	Gly	His	Leu	Gly	Tyr	Gln	Glu	Leu	Gly
705					710					715					720
Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys
				725					730				735		
Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln

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cont.

			740					745					750						
Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser				
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Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu				
		770				775						780							
His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu				
785					790					795					800				
Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala				
				805					810						815				
Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu				
			820					825					830						
Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys				
		835					840					845							
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		850				855						860							
Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr				
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Ser	Asn	Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile				
				885					890					895					
Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu				
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Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val				
		915					920					925							
Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro				
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Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg				
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Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn				
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Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr				
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Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro				
		995				1000					1005								
Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln				
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Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu				
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Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu				
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Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala				
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		1090				1095					1100								
Val	Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala				
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Gly	Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro				
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Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys				
		1140					1145					1150							
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Ile	Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys				
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Ser	Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser				
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a26
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 Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr
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 1265 1270 1275 1280
 Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys
 1285 1290 1295
 Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala
 1300 1305 1310
 Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His
 1315 1320 1325
 Ser Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu
 1330 1335 1340
 Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser
 1345 1350 1355 1360
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 1365 1370 1375
 Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln
 1380 1385 1390
 Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg
 1395 1400 1405
 Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp
 1410 1415 1420
 Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys
 1425 1430 1435 1440
 Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met
 1445 1450 1455
 Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His
 1460 1465 1470
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 1475 1480 1485
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 1490 1495 1500
 Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val
 1505 1510 1515 1520
 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
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 Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
 1540 1545 1550
 Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp
 1555 1560 1565
 Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu
 1570 1575 1580
 Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu
 1585 1590 1595 1600
 Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
 1605 1610 1615
 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
 1620 1625 1630
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 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp
 1650 1655 1660
 Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe
 1665 1670 1675 1680
 Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr
 1685 1690 1695
 Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys
 1700 1705 1710
 Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn

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 int.

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 Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val
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 Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe
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 Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr
 1765 1770 1775
 Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg
 1780 1785 1790
 Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile
 1795 1800 1805
 Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala
 1810 1815 1820
 Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser
 1825 1830 1835 1840
 Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser
 1845 1850 1855
 Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe
 1860 1865 1870
 Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu
 1875 1880 1885
 Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu
 1890 1895 1900
 Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu
 1905 1910 1915 1920
 Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile
 1925 1930 1935
 Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro
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 1955 1960 1965
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tcc 183

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ttgcttctct tttcactcta gatttaa 147

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<212> DNA
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<220>
<223> Exon 5

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tgaccatgag ggtgaggacg cacatcactt tgccctcccc tctcacaagc cctttc 176

<210> 125
<211> 206
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 6

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gattcaactt ggcgatggat cctataattt gaatttttat aaagatgaaa agatctccaa 120
agaaccaaaa ggatcaatat ttctggattc ctgtatgggt gtcgttcagg taaatatgaa 180
aagagtttta ccattatggt ttctta 206

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<213> Homo sapiens

<220>
<223> Exon 7

<400> 126
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aagaatggat cacaattcta aataagatcc tccagctcaa ctttgaagct gcaatgcaag 180
aaaagcgaaa tggcgactct cacgaaggta gataggcttg gcttccccca ggcacataca 240
cactct 246

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<212> DNA
<213> Homo sapiens

<220>
<223> Exon 8

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tatcttctgc tcttcgttga atgc 144

Q46
unt:
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actatctaaa tgtttaatat ttaaaaccaa at 152

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ttatctttca atttgcaatg ctgtgttgcc gaaaatgaag aaggaccacac taaaaatgta 180
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<211> 289

<212> DNA
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<220>
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atctctcagt gaggcaaag ctcgccacca cgtccccggc gctgatgaat ggcagtgggc 180
agagcccatc tgcctcaag ggcattcttc atgaagccgc catgcagtat ccgaagcagg 240
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<211> 205
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<220>
<223> Exon 12

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<212> DNA
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<210> 133
<211> 159
<212> DNA
<213> Homo sapiens

<220>
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<400> 133
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<212> DNA
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<220>

<223> Genomic DNA at the CLASP-2 locus.

<400> 134

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Q26
cont.

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 <213> Homo sapiens

<220>
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<400> 135

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 35 40 45
 Val Val Asn Tyr Lys Tyr Glu Asp Phe Ser Gly Asp Phe Arg Met Leu
 50 55 60
 Pro Cys Lys Ser Leu Arg Pro Glu Lys Ile Pro Asn His Val Phe Glu
 65 70 75 80
 Ile Asp Glu Asp Cys Glu Lys Asp Glu Asp Ser Ser Ser Leu Cys Ser
 85 90 95
 Gln Lys Gly Gly Val Ile Lys Gln Gly Trp Leu His Lys Ala Asn Val
 100 105 110
 Asn Ser Thr Ile Thr Val Thr Met Lys Val Phe Lys Arg Arg Tyr Phe
 115 120 125
 Tyr Leu Thr Gln Leu Pro Asp Gly Ser Tyr Ile Leu Asn Ser Tyr Lys
 130 135 140
 Asp Glu Lys Asn Ser Lys Glu Ser Lys Gly Cys Ile Tyr Leu Asp Ala
 145 150 155 160
 Cys Ile Asp Val Val Gln Cys Pro Lys Met Arg Arg His Ala Phe Glu
 165 170 175
 Leu Lys Met Leu Asp Lys Tyr Ser His Tyr Leu Ala Ala Glu Thr Glu
 180 185 190
 Gln Glu Met Glu Glu Trp Leu Ile Thr Leu Lys Lys Ile Ile Gln Ile
 195 200 205
 Asn Thr Asp Ser Leu Val Gln Glu Lys Lys Glu Thr Val Glu Thr Ala
 210 215 220
 Gln Asp Asp Glu Thr Ser Ser Gln Gly Lys Ala Glu Asn Ile Met Ala
 225 230 235 240
 Ser Leu Glu Arg Ser Met His Pro Glu Leu Met Lys Tyr Gly Arg Glu
 245 250 255
 Thr Glu Gln Leu Asn Lys Leu Ser Arg Gly Asp Gly Arg Gln Asn Leu
 260 265 270

Q26
 cont.

Phe Ser Phe Asp Ser Glu Val Gln Arg Leu Asp Phe Ser Gly Ile Glu
 275 280 285
 Pro Asp Ile Lys Pro Phe Glu Glu Lys Cys Asn Lys Arg Phe Leu Val
 290 295 300
 Asn Cys His Asp Leu Thr Phe Asn Ile Leu Gly Gln Ile Gly Asp Asn
 305 310 315 320
 Ala Lys Gly Pro Pro Thr Asn Val Glu Pro Phe Phe Ile Asn Leu Ala
 325 330 335
 Leu Phe Asp Val Lys Asn Asn Cys Lys Ile Ser Ala Asp Phe His Val
 340 345 350
 Asp Leu Asn Pro Pro Ser Val Arg Glu Met Leu Trp Gly Ser Ser Thr
 355 360 365
 Gln Leu Ala Ser Asp Gly Ser Pro Lys Gly Ser Ser Pro Glu Ser Tyr
 370 375 380
 Ile His Gly Ile Ala Glu Ser Gln Leu Arg Tyr Ile Gln Gln Gly Ile
 385 390 395 400
 Phe Ser Val Thr Asn Pro His Pro Glu Ile Phe Leu Val Ala Arg Ile
 405 410 415
 Glu Lys Val Leu Gln Gly Asn Ile Thr His Cys Ala Glu Pro Tyr Ile
 420 425 430
 Lys Asn Ser Asp Pro Val Lys Thr Ala Gln Lys Val His Arg Thr Ala
 435 440 445
 Lys Gln Val Cys Ser Arg Leu Gly Gln Tyr Arg Met Pro Phe Ala Trp
 450 455 460
 Ala Ala Arg Pro Ile Phe Lys Asp Thr Gln Gly Ser Leu Asp Leu Asp
 465 470 475 480
 Gly Arg Phe Ser Pro Leu Tyr Lys Gln Asp Ser Ser Lys Leu Ser Ser
 485 490 495
 Glu Asp Ile Leu Lys Leu Leu Ser Glu Tyr Lys Lys Pro Glu Lys Thr
 500 505 510
 Lys Leu Gln Ile Ile Pro Gly Gln Leu Asn Ile Thr Val Glu Cys Val
 515 520 525
 Pro Val Asp Leu Ser Asn Cys Ile Thr Ser Ser Tyr Val Pro Leu Lys
 530 535 540
 Pro Phe Glu Lys Asn Cys Gln Asn Ile Thr Val Glu Val Glu Glu Phe
 545 550 555 560
 Val Pro Glu Met Thr Lys Tyr Cys Tyr Pro Phe Thr Ile Tyr Lys Asn
 565 570 575
 His Leu Tyr Val Tyr Pro Leu Gln Leu Lys Tyr Asp Ser Gln Lys Thr
 580 585 590
 Phe Ala Lys Ala Arg Asn Ile Ala Val Cys Val Glu Phe Arg Asp Ser

926
 cont.

595 600 605

Asp Glu Ser Asp Ala Ser Ala Leu Lys Cys Ile Tyr Gly Lys Pro Ala
610 615 620

Gly Ser Val Phe Thr Thr Asn Ala Tyr Ala Val Val Ser His His Asn
625 630 635 640

Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile Glu Leu Pro Ile His
645 650 655

Leu His Gln Lys His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys
660 665 670

Glu Ile Asn Thr Lys Gly Thr Thr Lys Lys Gln Asp Thr Val Glu Thr
675 680 685

Pro Val Gly Phe Ala Trp Val Pro Leu Leu Lys Asp Gly Arg Ile Ile
690 695 700

Thr Phe Glu Gln Gln Leu Pro Val Ser Ala Asn Leu Pro Pro Gly Tyr
705 710 715 720

Leu Asn Leu Asn Asp Ala Glu Ser Arg Arg Gln Cys Asn Val Asp Ile
725 730 735

Lys Trp Val Asp Gly Ala Lys Pro Leu Leu Lys Phe Lys Ser His Leu
740 745 750

Glu Ser Thr Ile Tyr Thr Gln Asp Leu His Val His Lys Phe Phe His
755 760 765

His Cys Gln Leu Ile Gln Ser Gly Ser Lys Glu Val Pro Gly Glu Leu
770 775 780

Ile Lys Tyr Leu Lys Cys Leu His Ala Met Glu Ile Gln Val Met Ile
785 790 795 800

Gln Phe Leu Pro Val Ile Leu Met Gln Leu Phe Arg Val Leu Thr Asn
805 810 815

Met Thr His Glu Asp Asp Val Pro Ile Asn Cys Thr Met Val Leu Leu
820 825 830

His Ile Val Ser Lys Cys His Glu Glu Gly Leu Asp Ser Tyr Leu Arg
835 840 845

Ser Phe Ile Lys Tyr Ser Phe Arg Pro Glu Lys Pro Ser Ala Pro Gln
850 855 860

Ala Gln Leu Ile His Glu Thr Leu Ala Thr Thr Met Ile Ala Ile Leu
865 870 875 880

Lys Gln Ser Ala Asp Phe Leu Ser Ile Asn Lys Leu Leu Lys Tyr Ser
885 890 895

Trp Phe Phe Phe Glu Ile Ile Ala Lys Ser Met Ala Thr Tyr Leu Leu
900 905 910

Glu Glu Asn Lys Ile Lys Leu Pro Arg Gly Gln Arg Phe Pro Glu Thr
915 920 925

926
cont.

Tyr His His Val Leu His Ser Leu Leu Leu Ala Ile Ile Pro His Val
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 Ser Leu Ala Ser Phe Leu Lys Arg Cys Leu Thr Leu Met Asp Arg Gly
 965 970 975
 Phe Ile Phe Asn Leu Ile Asn Asp Tyr Ile Ser Gly Phe Ser Pro Lys
 980 985 990
 Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe Glu Phe Leu Gln Thr Ile
 995 1000 1005
 Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro Met Ala Phe Ala
 1010 1015 1020
 Lys Pro Lys Leu Gln Arg Val Gln Asp Ser Asn Leu Glu Tyr Ser Leu
 1025 1030 1035 1040
 Ser Asp Glu Tyr Cys Lys His His Phe Leu Val Gly Leu Leu Leu Arg
 1045 1050 1055
 Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr Glu Ile Arg Tyr Thr Ala
 1060 1065 1070
 Ile Ser Val Ile Lys Asn Leu Leu Ile Lys His Ala Phe Asp Thr Arg
 1075 1080 1085
 Tyr Gln His Lys Asn Gln Gln Ala Lys Ile Ala Gln Leu Tyr Leu Pro
 1090 1095 1100
 Phe Val Gly Leu Leu Leu Glu Asn Ile Gln Arg Leu Ala Gly Arg Asp
 1105 1110 1115 1120
 Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn Ser Ala Ser Arg Asp Glu
 1125 1130 1135
 Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn Arg Gly Ser Leu Ser Thr
 1140 1145 1150
 Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln Asn Gly His Gly Ile Lys
 1155 1160 1165
 Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro Glu Gly Ala Thr Gly Phe
 1170 1175 1180
 Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr Arg Gln Ser Ser Thr Arg
 1185 1190 1195 1200
 Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp Gln Tyr Glu Ile Arg Ser
 1205 1210 1215
 Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys Met Ile Ser Glu Asp Thr
 1220 1225 1230
 Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro Gln Glu Leu Ile Asn Ile
 1235 1240 1245

026
 end-

Leu Ile Leu Leu Glu Val Cys Leu Phe His Phe Arg Tyr Met Gly Lys
1250 1255 1260

Arg Asn Ile Ala Arg Val His Asp Ala Trp Leu Ser Lys His Phe Gly
1265 1270 1275 1280

Ile Asp Arg Lys Ser Gln Thr Met Pro Ala Leu Arg Asn Arg Ser Gly
1285 1290 1295

Val Met Gln Ala Arg Leu Gln His Leu Ser Ser Leu Glu Ser Ser Phe
1300 1305 1310

Thr Leu Asn His Ser Ser Thr Thr Thr Glu Ala Asp Ile Phe His Gln
1315 1320 1325

Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu Val Ser Leu Thr Val Leu
1330 1335 1340

Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe Lys Thr Gln Leu Leu Asn
1345 1350 1355 1360

Asn Asp Gly His Asn Pro Leu Met Lys Lys Val Phe Asp Ile His Leu
1365 1370 1375

Ala Phe Leu Lys Asn Gly Gln Ser Glu Val Ser Leu Lys His Val Phe
1380 1385 1390

Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe Pro Ser Ala Phe Phe Lys
1395 1400 1405

Gly Arg Val Asn Met Cys Ala Ala Phe Cys Tyr Glu Val Leu Lys Cys
1410 1415 1420

Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn Glu Ala Ser Ala Leu Leu
1425 1430 1435 1440

Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr Thr Lys Arg Lys Thr Phe
1445 1450 1455

Leu Arg Thr His Leu Gln Ile Ile Ile Ala Val Ser Gln Leu Ile Ala
1460 1465 1470

Asp Val Ala Leu Ser Gly Gly Ser Arg Phe Gln Glu Ser Leu Phe Ile
1475 1480 1485

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1490 1495 1500

Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met
1505 1510 1515 1520

Ala Thr Ala Gln Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Ile
1525 1530 1535

Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu
1540 1545 1550

Arg Lys Thr Trp Leu Asp Ser Met Ala Lys Ile His Val Lys Asn Gly
1555 1560 1565

Asp Phe Ser Glu Ala Ala Met Cys Tyr Val His Val Ala Ala Leu Val

Q26
end.

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Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu Glu Gly Ala Met Lys Glu		
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Asp Ala Gly Met Met Asp Val His Tyr Ser Glu Glu Val Leu Leu Glu		
	1620	1625 1630
Leu Leu Glu Gln Cys Val Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu		
	1635	1640 1645
Ile Ile Ser Glu Ile Ser Lys Leu Ile Val Pro Ile Tyr Glu Lys Arg		
	1650	1655 1660
Arg Glu Phe Glu Lys Leu Thr Gln Val Tyr Arg Thr Leu His Gly Ala		
1665	1670	1675 1680
Tyr Thr Lys Ile Leu Glu Val Met His Thr Lys Lys Arg Leu Leu Gly		
	1685	1690 1695
Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu		
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Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser		
	1715	1720 1725
Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr Gly Glu Lys Phe Gly Thr		
	1730	1735 1740
Glu Asn Val Lys Ile Ile Gln Asp Ser Asp Lys Val Asn Ala Lys Glu		
1745	1750	1755 1760
Leu Asp Pro Lys Tyr Ala His Ile Gln Val Thr Tyr Val Lys Pro Tyr		
	1765	1770 1775
Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys Thr Glu Phe Glu Arg Asn		
	1780	1785 1790
His Asn Ile Ser Arg Phe Val Phe Glu Ala Pro Tyr Thr Leu Ser Gly		
	1795	1800 1805
Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu		
	1810	1815 1820
Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg Ile Pro Ile Asn		
1825	1830	1835 1840
Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Gly Ala Thr Asp Glu		
	1845	1850 1855
Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys Leu Cys Ser Ser Thr Asp		
	1860	1865 1870
Val Asp Met Ile Gln Leu Gln Leu Lys Leu Gln Gly Trp Val Ser Val		
	1875	1880 1885
Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp		
1890	1895	1900

all
cont.

Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp
 1905 1910 1915 1920

Met Phe Arg Lys Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu Leu Asn
 1925 1930 1935

Glu Arg Leu Ile Lys Glu Asp Gln Val Glu Tyr His Glu Gly Leu Lys
 1940 1945 1950

Ser Asn Phe Arg Asp Met Val Lys Glu Leu Ser Asp Ile Ile His Glu
 1955 1960 1965

Gln Ile Leu Gln Glu Asp Thr Met His Ser Pro Trp Met Ser Asn Thr
 1970 1975 1980

Leu His Val Phe Cys Ala Ile Ser Gly Thr Ser Ser Asp Arg Gly Tyr
 1985 1990 1995 2000

Gly Ser Pro Arg Tyr Ala Glu Val
 2005

<210> 136
 <211> 2015
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CLASP-5 amino acid sequence

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Arg Thr Leu Gln Pro Ser Leu Pro Glu Glu Gly Val Glu Leu Asp Pro
 35 40 45

His Val Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val
 50 55 60

Asn Arg Lys Asn Gln Gly Ser Pro Glu Ile Cys Gly Phe Lys Lys Thr
 65 70 75 80

Gly Ser Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu
 85 90 95

Ser Glu Thr Leu Glu Cys Ser Glu Pro Ala Ala Gln Ala Gly Pro Arg
 100 105 110

His Leu Asn Val Leu Cys Asp Val Ser Gly Lys Gly Pro Val Thr Ala
 115 120 125

Cys Asp Phe Asp Leu Arg Ser Leu Gln Pro Asp Lys Arg Leu Glu Asn
 130 135 140

Leu Leu Gln Gln Val Ser Ala Glu Asp Phe Glu Lys Gln Asn Glu Glu
 145 150 155 160

Ala Arg Arg Thr Asn Arg Gln Ala Glu Leu Phe Ala Leu Tyr Pro Ser
 165 170 175
 Val Asp Glu Glu Asp Ala Val Glu Ile Arg Pro Val Pro Glu Cys Pro
 180 185 190
 Lys Glu His Leu Gly Asn Arg Ile Leu Val Lys Leu Leu Thr Leu Lys
 195 200 205
 Phe Glu Ile Glu Ile Glu Pro Leu Phe Ala Ser Ile Ala Leu Tyr Asp
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 Val Lys Glu Arg Lys Lys Ile Ser Glu Asn Phe His Cys Asp Leu Asn
 225 230 235 240
 Ser Asp Gln Phe Lys Gly Phe Leu Arg Ala His Thr Pro Ser Val Ala
 245 250 255
 Ala Ser Ser Gln Ala Arg Ser Ala Val Phe Ser Val Thr Tyr Pro Ser
 260 265 270
 Ser Asp Ile Tyr Leu Val Val Lys Ile Glu Lys Val Leu Gln Gln Gly
 275 280 285
 Asp Ile Gly Asp Cys Ala Glu Pro Tyr Thr Val Ile Lys Glu Ser Asp
 290 295 300
 Gly Gly Lys Ser Lys Glu Lys Ile Glu Lys Leu Lys Leu Gln Ala Glu
 305 310 315 320
 Ser Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp Ala
 325 330 335
 Pro Ile Ser Leu Ser Ser Phe Phe Asn Val Ser Thr Leu Glu Arg Glu
 340 345 350
 Val Thr Asp Val Asp Ser Val Val Gly Arg Ser Pro Val Gly Glu Arg
 355 360 365
 Arg Thr Leu Ala Gln Ser Arg Arg Leu Ser Glu Arg Ala Leu Ser Leu
 370 375 380
 Glu Glu Asn Gly Val Gly Ser Asn Phe Lys Thr Ser Thr Leu Ser Val
 385 390 395 400
 Ser Ser Phe Phe Lys Gln Glu Gly Asp Arg Leu Ser Asp Glu Asp Leu
 405 410 415
 Phe Lys Phe Leu Ala Asp Tyr Lys Arg Ser Ser Ser Leu Gln Arg Arg
 420 425 430
 Val Lys Ser Ile Pro Gly Leu Leu Arg Leu Glu Ile Ser Thr Ala Pro
 435 440 445
 Glu Ile Ile Asn Cys Cys Leu Thr Pro Glu Met Leu Pro Val Lys Pro
 450 455 460
 Phe Pro Glu Asn Arg Thr Arg Pro His Lys Glu Ile Leu Glu Phe Pro
 465 470 475 480

Q26
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Thr	Arg	Glu	Val	Tyr	Val	Pro	His	Thr	Val	Tyr	Arg	Asn	Leu	Leu	Tyr			
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Asn	Ile	Thr	Ile	Lys	Ile	Gln	Phe	Met	Cys	Gly	Glu	Asp	Ala	Ser	Asn			
		515					520					525						
Ala	Met	Pro	Val	Ile	Phe	Gly	Lys	Ser	Ser	Gly	Pro	Glu	Phe	Leu	Gln			
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Glu	Val	Tyr	Thr	Ala	Val	Thr	Tyr	His	Asn	Lys	Ser	Pro	Asp	Phe	Tyr			
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Glu	Glu	Val	Lys	Ile	Lys	Leu	Pro	Ala	Lys	Leu	Thr	Val	Asn	His	His			
				565					570					575				
Leu	Leu	Phe	Thr	Phe	Tyr	His	Ile	Ser	Cys	Gln	Gln	Lys	Gln	Gly	Ala			
			580					585					590					
Ser	Val	Glu	Thr	Leu	Leu	Gly	Tyr	Ser	Trp	Leu	Pro	Ile	Leu	Leu	Asn			
		595					600					605						
Glu	Arg	Leu	Gln	Thr	Gly	Ser	Tyr	Cys	Leu	Pro	Val	Ala	Leu	Glu	Lys			
	610					615					620							
Leu	Pro	Pro	Asn	Tyr	Ser	Met	His	Ser	Ala	Glu	Lys	Val	Pro	Leu	Gln			
625					630					635					640			
Asn	Pro	Pro	Ile	Lys	Trp	Ala	Glu	Gly	His	Lys	Gly	Val	Phe	Asn	Ile			
				645					650					655				
Glu	Val	Gln	Ala	Val	Ser	Ser	Val	His	Thr	Gln	Asp	Asn	His	Leu	Glu			
			660					665					670					
Lys	Phe	Phe	Thr	Leu	Cys	His	Ser	Leu	Glu	Ser	Gln	Val	Thr	Phe	Pro			
		675					680					685						
Ile	Arg	Val	Leu	Asp	Gln	Lys	Ile	Ser	Glu	Met	Ala	Leu	Glu	His	Glu			
	690					695				700								
Leu	Lys	Leu	Ser	Ile	Ile	Cys	Leu	Asn	Ser	Ser	Arg	Leu	Glu	Pro	Leu			
705					710					715					720			
Val	Leu	Phe	Leu	His	Leu	Val	Leu	Asp	Lys	Leu	Phe	Gln	Leu	Ser	Val			
				725					730					735				
Gln	Pro	Met	Val	Ile	Ala	Gly	Gln	Thr	Ala	Asn	Phe	Ser	Gln	Phe	Ala			
			740					745					750					
Phe	Glu	Ser	Val	Val	Ala	Ile	Ala	Asn	Ser	Leu	His	Asn	Ser	Lys	Asp			
		755					760					765						
Leu	Ser	Lys	Asp	Gln	His	Gly	Arg	Asn	Cys	Leu	Leu	Ala	Ser	Tyr	Val			
	770					775					780							
His	Tyr	Val	Phe	Arg	Leu	Pro	Glu	Val	Gln	Arg	Asp	Val	Pro	Lys	Ser			
785					790					795					800			
Gly	Ala	Pro	Thr	Ala	Leu	Leu	Asp	Pro	Arg	Ser	Tyr	His	Thr	Tyr	Gly			

a26
end.

805 810 815
 Arg Thr Ser Ala Ala Ala Val Ser Ser Lys Leu Leu Gln Ala Arg Val
 820 825 830
 Met Ser Ser Ser Asn Pro Asp Leu Ala Gly Thr His Ser Ala Ala Asp
 835 840 845
 Glu Glu Val Lys Asn Ile Met Ser Ser Lys Ile Ala Asp Arg Asn Cys
 850 855 860
 Ser Arg Met Ser Tyr Tyr Cys Ser Gly Ser Ser Asp Ala Pro Ser Ser
 865 870 875 880
 Pro Ala Ala Pro Arg Pro Ala Ser Lys Lys His Phe His Glu Glu Leu
 885 890 895
 Ala Leu Gln Met Val Val Ser Thr Gly Met Val Lys Ser Met Ala Gln
 900 905 910
 His Val His Asn Met Asp Lys Arg Asp Ser Phe Arg Arg Thr Arg Phe
 915 920 925
 Ser Asp Arg Phe Met Asp Asp Ile Thr Thr Ile Val Asn Val Val Thr
 930 935 940
 Ser Glu Ile Ala Ala Leu Leu Val Lys Pro Gln Lys Glu Asn Glu Gln
 945 950 955 960
 Ala Glu Lys Met Asn Ile Ser Leu Ala Phe Phe Leu Tyr Asp Leu Leu
 965 970 975
 Ser Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Arg His Tyr Cys
 980 985 990
 Ser Gln Leu Ser Ala Lys Leu Ser Asn Leu Pro Thr Leu Ile Ser Met
 995 1000 1005
 Arg Leu Glu Phe Leu Arg Ile Leu Cys Ser His Glu His Tyr Leu Asn
 1010 1015 1020
 Leu Asn Leu Phe Phe Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys
 1025 1030 1035 1040
 Pro Ser Ile Ser Ser Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp
 1045 1050 1055
 Gln Lys Ile Ala Ser Met Phe Asp Leu Thr Ser Glu Tyr Arg Gln Gln
 1060 1065 1070
 His Phe Leu Thr Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp
 1075 1080 1085
 Ala Glu Gly Glu Gly Ile Ser Lys Val Gln Arg Lys Ala Val Ser Ala
 1090 1095 1100
 Ile His Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys
 1105 1110 1115 1120
 Pro Glu Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly
 1125 1130 1135

a26
 cont.

Ile Ile Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp
 1140 1145 1150
 Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala
 1155 1160 1165
 Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe
 1170 1175 1180
 Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln
 1185 1190 1195 1200
 Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe
 1205 1210 1215
 Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile
 1220 1225 1230
 Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe
 1235 1240 1245
 Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys
 1250 1255 1260
 Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu
 1265 1270 1275 1280
 Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg
 1285 1290 1295
 Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu
 1300 1305 1310
 Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu
 1315 1320 1325
 Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn
 1330 1335 1340
 Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile
 1345 1350 1355 1360
 Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly
 1365 1370 1375
 Val Leu Arg Val Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr
 1380 1385 1390
 Tyr Leu Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe
 1395 1400 1405
 Gly Asp Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys
 1410 1415 1420
 His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser
 1425 1430 1435 1440
 Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala
 1445 1450 1455

976
 cont.

Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala
 1460 1465 1470
 Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg
 1475 1480 1485
 Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln
 1490 1495 1500
 Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn
 1505 1510 1515 1520
 Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro
 1525 1530 1535
 Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala
 1540 1545 1550
 Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His
 1555 1560 1565
 Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala
 1570 1575 1580
 Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr
 1585 1590 1595 1600
 Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu
 1605 1610 1615
 Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly
 1620 1625 1630
 Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu
 1635 1640 1645
 Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val
 1650 1655 1660
 Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu
 1665 1670 1675 1680
 Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp
 1685 1690 1695
 Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg
 1700 1705 1710
 Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe
 1715 1720 1725
 Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg
 1730 1735 1740
 Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val
 1745 1750 1755 1760
 Ile Lys Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys
 1765 1770 1775
 Ala Tyr Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu

1780	1785	1790
Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg 1795	1800	1805
Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu 1810	1815	1820
Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala 1825	1830	1835 1840
Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe 1845	1850	1855
Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr 1860	1865	1870
Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met 1875	1880	1885
Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly 1890	1895	1900
Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro 1905	1910	1915 1920
Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe 1925	1930	1935
Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr 1940	1945	1950
Ala Asp Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys 1955	1960	1965
Leu Lys Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu 1970	1975	1980
Tyr Lys Pro Ile Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His 1985	1990	1995 2000
Arg Ser Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser 2005	2010	2015

<210> 137

<211> 2090

<212> PRT

<213> Homo sapiens

<220>

<223> CLASP-3 amino acid sequence

<400> 137

Met	Ala	Glu	Arg	Arg	Ala	Phe	Ala	Gln	Lys	Ile	Ser	Arg	Thr	Val	Ala
1				5					10					15	

Ala	Glu	Val	Arg	Lys	Gln	Ile	Ser	Gly	Gln	Tyr	Ser	Gly	Ser	Pro	Gln
		20						25					30		

Leu Leu Lys Asn Leu Asn Ile Val Gly Asn Ile Ser His His Thr Thr

35					40					45					
Val	Pro	Leu	Thr	Glu	Ala	Val	Asp	Pro	Val	Asp	Leu	Glu	Asp	Tyr	Leu
	50					55					60				
Ile	Thr	His	Pro	Leu	Ala	Val	Asp	Ser	Gly	Pro	Leu	Arg	Asp	Leu	Ile
65					70					75					80
Glu	Phe	Pro	Pro	Asp	Asp	Ile	Glu	Val	Val	Tyr	Ser	Pro	Arg	Asp	Cys
				85					90					95	
Arg	Thr	Leu	Val	Ser	Ala	Val	Pro	Glu	Glu	Ser	Glu	Met	Asp	Pro	His
			100					105					110		
Val	Arg	Asp	Cys	Ile	Arg	Ser	Tyr	Thr	Glu	Asp	Trp	Ala	Ile	Val	Ile
		115					120					125			
Arg	Lys	Tyr	His	Lys	Leu	Gly	Thr	Gly	Phe	Asn	Pro	Asn	Thr	Leu	Asp
	130					135					140				
Lys	Gln	Lys	Glu	Arg	Gln	Lys	Gly	Leu	Pro	Lys	Gln	Val	Phe	Glu	Ser
145					150					155					160
Asp	Glu	Ala	Pro	Asp	Gly	Asn	Ser	Tyr	Gln	Asp	Asp	Gln	Asp	Asp	Leu
				165					170					175	
Lys	Arg	Arg	Ser	Met	Ser	Ile	Asp	Asp	Thr	Pro	Arg	Gly	Ser	Trp	Ala
			180					185					190		
Cys	Ser	Ile	Phe	Asp	Leu	Lys	Asn	Ser	Leu	Pro	Asp	Ala	Leu	Leu	Pro
		195					200					205			
Asn	Leu	Leu	Asp	Arg	Thr	Pro	Asn	Glu	Glu	Ile	Asp	Arg	Gln	Asn	Asp
	210					215					220				
Asp	Gln	Arg	Lys	Ser	Asn	Arg	His	Lys	Glu	Leu	Phe	Ala	Leu	His	Pro
225					230					235					240
Ser	Pro	Asp	Glu	Glu	Glu	Pro	Ile	Glu	Arg	Leu	Ser	Val	Pro	Asp	Ile
				245					250					255	
Pro	Lys	Glu	His	Phe	Gly	Gln	Arg	Leu	Leu	Val	Lys	Cys	Leu	Ser	Leu
			260					265					270		
Lys	Phe	Glu	Ile	Glu	Ile	Glu	Pro	Ile	Phe	Ala	Ser	Leu	Ala	Leu	Tyr
		275					280					285			
Asp	Val	Lys	Glu	Lys	Lys	Lys	Ile	Ser	Glu	Asn	Phe	Tyr	Phe	Asp	Leu
	290					295					300				
Asn	Ser	Glu	Gln	Met	Lys	Gly	Leu	Leu	Arg	Pro	His	Val	Pro	Pro	Ala
305					310					315					320
Ala	Ile	Thr	Thr	Leu	Ala	Arg	Ser	Ala	Ile	Phe	Ser	Ile	Thr	Tyr	Pro
				325					330					335	
Ser	Gln	Asp	Val	Phe	Leu	Val	Ile	Lys	Leu	Glu	Lys	Val	Leu	Gln	Gln
			340					345					350		
Gly	Asp	Ile	Gly	Glu	Cys	Ala	Glu	Pro	Tyr	Met	Ile	Phe	Lys	Glu	Ala
		355					360					365			

026
cont.

Asp Ala Thr Lys Asn Lys Glu Lys Leu Glu Lys Leu Lys Ser Gln Ala
 370 375 380
 Asp Gln Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp
 385 390 395 400
 Thr Ala Ile His Leu Met Asn Ile Val Ser Ser Ala Gly Ser Leu Glu
 405 410 415
 Arg Asp Ser Thr Glu Val Glu Ile Ser Thr Gly Glu Arg Lys Gly Ser
 420 425 430
 Trp Ser Glu Arg Arg Asn Ser Ser Ile Val Gly Arg Arg Ser Leu Glu
 435 440 445
 Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn Leu Thr Ser Phe Arg Pro
 450 455 460
 Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Gly Asp Arg Leu
 465 470 475 480
 Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala Asp Met Arg Arg Pro Ser
 485 490 495
 Ser Val Leu Arg Arg Leu Arg Pro Ile Thr Ala Gln Leu Lys Ile Asp
 500 505 510
 Ile Ser Pro Ala Pro Glu Asn Pro His Tyr Cys Leu Thr Pro Glu Leu
 515 520 525
 Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg Val Arg Pro Thr Arg Glu
 530 535 540
 Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr Val Pro Asn Thr Thr Tyr
 545 550 555 560
 Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser Leu Asn Phe Ala Asn Arg
 565 570 575
 Gln Gly Ser Ala Arg Asn Ile Thr Val Lys Val Gln Phe Met Tyr Gly
 580 585 590
 Glu Asp Pro Ser Asn Ala Met Pro Val Ile Phe Gly Lys Ser Ser Cys
 595 600 605
 Ser Glu Phe Ser Lys Glu Ala Tyr Thr Ala Val Val Tyr His Asn Arg
 610 615 620
 Ser Pro Asp Phe His Glu Glu Ile Lys Val Lys Leu Pro Ala Thr Leu
 625 630 635 640
 Thr Asp His His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys Gln
 645 650 655
 Gln Lys Gln Asn Thr Pro Leu Glu Thr Pro Val Gly Tyr Thr Trp Ile
 660 665 670
 Pro Met Leu Gln Asn Gly Arg Leu Lys Thr Gly Gln Phe Cys Leu Pro
 675 680 685

026
 cont.

Val	Ser	Leu	Glu	Lys	Pro	Pro	Gln	Ala	Tyr	Ser	Val	Leu	Ser	Pro	Glu
690						695					700				
Val	Pro	Leu	Pro	Gly	Met	Lys	Trp	Val	Asp	Asn	His	Lys	Gly	Val	Phe
705					710					715					720
Asn	Val	Glu	Val	Val	Ala	Val	Ser	Ser	Ile	His	Thr	Gln	Asp	Pro	Tyr
				725					730					735	
Leu	Asp	Lys	Phe	Phe	Ala	Leu	Val	Asn	Ala	Leu	Asp	Glu	His	Leu	Phe
			740					745					750		
Pro	Val	Arg	Ile	Gly	Asp	Met	Arg	Ile	Met	Glu	Asn	Asn	Leu	Glu	Asn
		755					760					765			
Glu	Leu	Lys	Ser	Ser	Ile	Ser	Ala	Leu	Asn	Ser	Ser	Gln	Leu	Glu	Pro
		770				775						780			
Val	Val	Arg	Phe	Leu	His	Leu	Leu	Leu	Asp	Lys	Leu	Ile	Leu	Leu	Val
785					790					795					800
Ile	Arg	Pro	Pro	Val	Ile	Ala	Gly	Gln	Ile	Val	Asn	Leu	Gly	Gln	Ala
				805					810					815	
Ser	Phe	Glu	Ala	Met	Ala	Ser	Ile	Ile	Asn	Arg	Leu	His	Lys	Asn	Leu
			820					825					830		
Glu	Gly	Asn	His	Asp	Gln	His	Gly	Arg	Asn	Ser	Leu	Leu	Ala	Ser	Tyr
		835					840					845			
Ile	His	Tyr	Val	Phe	Arg	Leu	Pro	Asn	Thr	Tyr	Pro	Asn	Ser	Ser	Ser
		850				855					860				
Pro	Gly	Pro	Gly	Gly	Leu	Gly	Gly	Ser	Val	His	Tyr	Ala	Thr	Met	Ala
865					870					875					880
Arg	Ser	Ala	Val	Arg	Pro	Ala	Ser	Leu	Asn	Leu	Asn	Arg	Ser	Arg	Ser
				885					890					895	
Leu	Ser	Asn	Ser	Asn	Pro	Asp	Ile	Ser	Gly	Thr	Pro	Thr	Ser	Pro	Asp
			900					905					910		
Asp	Glu	Val	Arg	Ser	Ile	Ile	Gly	Ser	Lys	Gly	Leu	Asp	Arg	Ser	Asn
		915					920					925			
Ser	Trp	Val	Asn	Thr	Gly	Gly	Pro	Lys	Ala	Ala	Pro	Trp	Gly	Ser	Asn
		930				935					940				
Pro	Ser	Pro	Ser	Ala	Glu	Ser	Thr	Gln	Ala	Met	Asp	Arg	Ser	Cys	Asn
945					950					955					960
Arg	Met	Ser	Ser	His	Thr	Glu	Thr	Ser	Ser	Phe	Leu	Gln	Thr	Leu	Thr
				965					970					975	
Gly	Arg	Leu	Pro	Thr	Lys	Lys	Leu	Phe	His	Glu	Glu	Leu	Ala	Leu	Gln
			980					985					990		
Trp	Val	Val	Cys	Ser	Gly	Ser	Val	Arg	Glu	Ser	Ala	Leu	Gln	Gln	Ala
		995					1000					1005			
Trp	Phe	Phe	Phe	Glu	Leu	Met	Val	Lys	Ser	Met	Val	His	His	Leu	Tyr

Q26
unt.

Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu
 1345 1350 1355 1360
 Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys
 1365 1370 1375
 Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met
 1380 1385 1390
 Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln
 1395 1400 1405
 Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly
 1410 1415 1420
 Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr
 1425 1430 1435 1440
 His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile
 1445 1450 1455
 Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu
 1460 1465 1470
 Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr
 1475 1480 1485
 Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His
 1490 1495 1500
 Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala
 1505 1510 1515 1520
 Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu
 1525 1530 1535
 Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys
 1540 1545 1550
 Ser Ser Ser Ile Gly Thr Ile Arg Ser His Pro Ser Ala Ser Leu Tyr
 1555 1560 1565
 Leu Leu Met Arg Gln Asn Phe Glu Ile Gly Asn Asn Phe Ala Arg Val
 1570 1575 1580
 Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln
 1585 1590 1595 1600
 Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr
 1605 1610 1615
 Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln
 1620 1625 1630
 Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val
 1635 1640 1645
 Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met
 1650 1655 1660

Q26
 26

Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp
 1665 1670 1675 1680
 Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu
 1685 1690 1695
 Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu
 1700 1705 1710
 Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe
 1715 1720 1725
 Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp
 1730 1735 1740
 Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr
 1745 1750 1755 1760
 Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser
 1765 1770 1775
 Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile
 1780 1785 1790
 Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His
 1795 1800 1805
 Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly
 1810 1815 1820
 Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr
 1825 1830 1835 1840
 Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala
 1845 1850 1855
 Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly
 1860 1865 1870
 Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro
 1875 1880 1885
 Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr
 1890 1895 1900
 Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr
 1905 1910 1915 1920
 Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro
 1925 1930 1935
 Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys
 1940 1945 1950
 Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr
 1955 1960 1965
 Arg Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu
 1970 1975 1980
 Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala

1985	1990	1995	2000
Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln			
2005	2010	2015	
Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln			
2020	2025	2030	
Val Phe Leu Ser Glu Ile Pro Ser Asp Pro Lys Leu Phe Arg His His			
2035	2040	2045	
Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp			
2050	2055	2060	
Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr			
2065	2070	2075	2080
Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro			
2085	2090		

<210> 138
 <211> 2047
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CLASP-7 amino acid sequence

<400> 138

all
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Met	Ala	Ala	Ser	Glu	Arg	Arg	Ala	Phe	Ala	His	Lys	Ile	Asn	Arg	Thr
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Val	Ala	Ala	Glu	Val	Arg	Lys	Gln	Val	Ser	Arg	Glu	Arg	Ser	Gly	Ser
			20					25					30		
Pro	His	Ser	Ser	Arg	Arg	Cys	Ser	Ser	Ser	Leu	Gly	Val	Pro	Leu	Thr
		35					40					45			
Glu	Val	Val	Glu	Pro	Leu	Asp	Phe	Glu	Asp	Val	Leu	Leu	Ser	Arg	Pro
	50					55					60				
Pro	Asp	Ala	Glu	Pro	Gly	Pro	Leu	Arg	Asp	Leu	Val	Glu	Phe	Pro	Ala
	65				70				75					80	
Asp	Asp	Leu	Glu	Leu	Leu	Leu	Gln	Pro	Arg	Glu	Cys	Arg	Thr	Thr	Glu
				85				90						95	
Pro	Gly	Ile	Pro	Lys	Asp	Glu	Lys	Leu	Asp	Ala	Gln	Val	Arg	Ala	Ala
			100					105					110		
Val	Glu	Met	Tyr	Ile	Glu	Asp	Trp	Val	Ile	Val	His	Arg	Arg	Tyr	Gln
		115					120					125			
Tyr	Leu	Ser	Ala	Ala	Tyr	Ser	Pro	Val	Thr	Thr	Asp	Thr	Gln	Arg	Glu
	130					135					140				
Arg	Gln	Lys	Gly	Leu	Pro	Arg	Gln	Val	Phe	Glu	Gln	Asp	Ala	Ser	Gly
145				150						155					160
Asp	Glu	Arg	Ser	Gly	Pro	Glu	Asp	Ser	Asn	Asp	Ser	Arg	Arg	Gly	Ser

165								170				175			
Gly	Ser	Pro	Glu	Asp	Thr	Pro	Arg	Ser	Ser	Gly	Ala	Ser	Ser	Ile	Phe
			180					185					190		
Asp	Leu	Arg	Asn	Leu	Ala	Ala	Asp	Ser	Leu	Leu	Pro	Ser	Leu	Leu	Glu
		195					200					205			
Arg	Ala	Ala	Pro	Glu	Asp	Val	Asp	Arg	Arg	Asn	Glu	Thr	Leu	Arg	Arg
	210					215					220				
Gln	His	Arg	Pro	Pro	Ala	Leu	Leu	Thr	Leu	Tyr	Pro	Ala	Pro	Asp	Glu
225					230					235					240
Asp	Glu	Ala	Val	Glu	Arg	Cys	Ser	Arg	Pro	Glu	Pro	Pro	Arg	Glu	His
				245					250					255	
Phe	Gly	Gln	Arg	Ile	Leu	Val	Lys	Cys	Leu	Ser	Leu	Lys	Phe	Glu	Ile
			260					265					270		
Glu	Ile	Glu	Pro	Ile	Phe	Gly	Ile	Leu	Ala	Leu	Tyr	Asp	Val	Arg	Glu
		275					280					285			
Lys	Lys	Lys	Ile	Ser	Glu	Asn	Phe	Tyr	Phe	Asp	Leu	Asn	Ser	Asp	Ser
	290					295					300				
Met	Lys	Gly	Leu	Leu	Arg	Ala	His	Gly	Thr	His	Pro	Ala	Ile	Ser	Thr
305					310					315					320
Leu	Ala	Arg	Ser	Ala	Ile	Phe	Ser	Val	Thr	Tyr	Pro	Ser	Pro	Asp	Ile
				325					330					335	
Phe	Leu	Val	Ile	Lys	Leu	Glu	Lys	Val	Leu	Gln	Gln	Gly	Asp	Ile	Ser
			340					345					350		
Glu	Cys	Cys	Glu	Pro	Tyr	Met	Val	Leu	Lys	Glu	Val	Asp	Thr	Ala	Lys
		355					360					365			
Asn	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Arg	Leu	Ala	Ala	Glu	Gln	Phe	Cys
	370					375					380				
Thr	Arg	Leu	Gly	Arg	Tyr	Arg	Met	Pro	Phe	Ala	Trp	Thr	Ala	Val	His
385					390					395					400
Leu	Ala	Asn	Ile	Val	Ser	Ser	Ala	Gly	Gln	Leu	Asp	Arg	Asp	Ser	Asp
				405					410					415	
Ser	Glu	Gly	Glu	Arg	Arg	Pro	Ala	Trp	Thr	Asp	Arg	Arg	Arg	Arg	Gly
			420					425					430		
Pro	Gln	Asp	Arg	Ala	Ser	Ser	Gly	Asp	Asp	Ala	Cys	Ser	Phe	Ser	Gly
		435					440					445			
Phe	Arg	Pro	Ala	Thr	Leu	Thr	Val	Thr	Asn	Phe	Phe	Lys	Gln	Glu	Ala
	450					455					460				
Glu	Arg	Leu	Ser	Asp	Glu	Asp	Leu	Phe	Lys	Phe	Leu	Ala	Asp	Met	Arg
465					470				475						480
Arg	Pro	Ser	Ser	Leu	Leu	Arg	Arg	Leu	Arg	Pro	Val	Thr	Ala	Gln	Leu
				485					490					495	

026
cont.

Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser
 500 505 510
 Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro
 515 520 525
 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His
 530 535 540
 Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe
 545 550 555 560
 Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg Val Gln Tyr
 565 570 575
 Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys
 580 585 590
 Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr
 595 600 605
 His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro
 610 615 620
 Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe Tyr His Val
 625 630 635 640
 Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe
 645 650 655
 Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe
 660 665 670
 Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr Ser Val Leu
 675 680 685
 Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp Gly His Lys
 690 695 700
 Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val His Pro Gln
 705 710 715 720
 Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val Leu Glu Glu
 725 730 735
 Gly Ala Phe Pro Phe Arg Leu Lys Asp Thr Val Leu Ser Glu Gly Asn
 740 745 750
 Val Glu Gln Glu Leu Arg Ala Ser Leu Ala Ala Leu Arg Leu Ala Ser
 755 760 765
 Pro Glu Pro Leu Val Ala Phe Ser His His Val Leu Asp Lys Leu Val
 770 775 780
 Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile Val Asn Leu
 785 790 795 800
 Gly Arg Gly Ala Phe Glu Ala Met Ala His Val Val Ser Leu Val His
 805 810 815

Arg Ser Leu Glu Ala Ala Gln Asp Ala Arg Gly His Cys Pro Gln Leu
 820 825 830
 Ala Ala Tyr Val His Tyr Ala Phe Arg Leu Pro Gly Thr Glu Pro Ser
 835 840 845
 Leu Pro Asp Gly Ala Pro Pro Val Thr Val Gln Ala Ala Thr Leu Ala
 850 855 860
 Arg Gly Ser Gly Arg Pro Ala Ser Leu Tyr Leu Ala Arg Ser Lys Ser
 865 870 875 880
 Ile Ser Ser Ser Asn Pro Asp Leu Ala Val Ala Pro Gly Ser Val Asp
 885 890 895
 Asp Glu Val Ser Arg Ile Leu Ala Ser Lys Leu Leu His Glu Glu Leu
 900 905 910
 Ala Leu Gln Trp Val Val Ser Ser Ser Ala Val Arg Glu Ala Ile Leu
 915 920 925
 Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser Met Ala Leu
 930 935 940
 His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys Leu Arg Phe
 945 950 955 960
 Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly Ser Val Gly
 965 970 975
 Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu Ala Glu His
 980 985 990
 Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val
 995 1000 1005
 Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val
 1010 1015 1020
 Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu
 1025 1030 1035 1040
 Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr
 1045 1050 1055
 Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro
 1060 1065 1070
 Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala
 1075 1080 1085
 Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg
 1090 1095 1100
 Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala
 1105 1110 1115 1120
 Leu Glu Pro Glu Ala Glu Gly Ala Phe Leu Leu His Lys Lys Ala Ile
 1125 1130 1135
 Ser Ala Val His Ser Leu Leu Cys Gly His Asp Thr Asp Pro Arg Tyr

1140	1145	1150
Ala Glu Ala Thr Val Lys Ala Arg Val Ala Glu Leu Tyr Leu Pro Leu 1155	1160	1165
Leu Ser Ile Ala Arg Asp Thr Leu Pro Arg Leu His Asp Phe Ala Glu 1170	1175	1180
Gly Pro Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr 1185	1190	1195 1200
Glu Gly Glu Gly Asp Ile Ala Gly Thr Ile Asn Pro Ser Val Ala Met 1205	1210	1215
Ala Ile Ala Gly Gly Pro Leu Ala Pro Gly Ser Arg Ala Ser Ile Ser 1220	1225	1230
Gln Gly Pro Pro Thr Ala Ser Arg Ala Gly Cys Ala Leu Ser Ala Glu 1235	1240	1245
Ser Ser Arg Thr Leu Leu Ala Cys Val Leu Trp Val Leu Lys Asn Thr 1250	1255	1260
Glu Pro Ala Leu Leu Gln Arg Trp Ala Thr Asp Leu Thr Leu Pro Gln 1265	1270	1275 1280
Leu Gly Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu 1285	1290	1295
Tyr Lys Gly Lys Lys Ala Phe Glu Arg Ile Asn Ser Leu Thr Phe Lys 1300	1305	1310
Lys Ser Leu Asp Met Lys Ala Arg Leu Glu Glu Ala Ile Leu Gly Thr 1315	1320	1325
Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg Glu Arg Ser Pro 1330	1335	1340
Phe Gly Asn Pro Glu Asn Val Arg Trp Arg Lys Ser Val Thr His Trp 1345	1350	1355 1360
Lys Gln Thr Ser Asp Arg Val Asp Lys Thr Lys Asp Glu Met Glu His 1365	1370	1375
Glu Ala Leu Val Glu Gly Asn Leu Ala Thr Glu Ala Ser Leu Val Val 1380	1385	1390
Leu Asp Thr Leu Glu Ile Ile Val Gln Thr Val Met Leu Ser Glu Ala 1395	1400	1405
Arg Glu Ser Val Leu Gly Ala Val Leu Lys Val Val Leu Tyr Ser Leu 1410	1415	1420
Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly Leu Ala Thr Gln 1425	1430	1435 1440
Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Asp Thr 1445	1450	1455
Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys Gly Ser 1460	1465	1470

Q26
cont.

Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu
 1475 1480 1485
 Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met
 1490 1495 1500
 Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr Gln Asn Phe
 1505 1510 1515 1520
 Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala
 1525 1530 1535
 Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu Gln Val Gln
 1540 1545 1550
 Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met
 1555 1560 1565
 Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg
 1570 1575 1580
 Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu
 1585 1590 1595 1600
 Gln Asn Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala
 1605 1610 1615
 Ala Gln Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala
 1620 1625 1630
 Leu Leu Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln
 1635 1640 1645
 Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile
 1650 1655 1660
 Leu Ser Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu
 1665 1670 1675 1680
 Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met
 1685 1690 1695
 Gly Gly Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro
 1700 1705 1710
 Ile Leu Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly
 1715 1720 1725
 Lys Leu Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp
 1730 1735 1740
 Glu Arg Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His
 1745 1750 1755 1760
 Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile
 1765 1770 1775
 Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu
 1780 1785 1790

a26
 cont.

Arg Phe Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val
 1795 1800 1805
 Asp Lys Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr
 1810 1815 1820
 Val Glu Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr
 1825 1830 1835 1840
 Phe Asp Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe
 1845 1850 1855
 Thr Pro Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg
 1860 1865 1870
 Lys Thr Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg
 1875 1880 1885
 Ile Arg Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val
 1890 1895 1900
 Ala Ile Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr
 1905 1910 1915 1920
 Glu Gln Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly
 1925 1930 1935
 Ser Val Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val
 1940 1945 1950
 Phe Leu Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn
 1955 1960 1965
 Lys Leu Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala
 1970 1975 1980
 Leu Arg Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His
 1985 1990 1995 2000
 Arg Glu Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro
 2005 2010 2015
 Leu Leu Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly
 2020 2025 2030
 Leu Arg Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu
 2035 2040 2045

<210> 139

<211> 2180

<212> PRT

<213> Homo sapiens

<220>

<223> CLASP-1 amino acid sequence

<400> 139

Met Ser Phe Arg Gly Lys Val Phe Lys Arg Glu Pro Ser Glu Phe Trp
 1 5 10 15

Lys Lys Arg Arg Thr Val Arg Arg Val Ile Gln Glu Glu Phe His Arg
 20 25 30
 Phe Ser Ser Gln Glu Lys Pro Arg Leu Leu Glu Pro Leu Asp Tyr Glu
 35 40 45
 Thr Val Ile Glu Glu Leu Glu Lys Thr Tyr Arg Asn Asp Pro Leu Gln
 50 55 60
 Asp Leu Leu Phe Phe Pro Ser Asp Asp Phe Ser Ala Ala Thr Val Ser
 65 70 75 80
 Trp Asp Ile Arg Thr Leu Tyr Ser Thr Val Pro Glu Asp Ala Glu His
 85 90 95
 Lys Ala Glu Asn Leu Leu Val Lys Glu Ala Cys Lys Phe Tyr Ser Ser
 100 105 110
 Gln Trp His Val Val Asn Tyr Lys Tyr Glu Gln Tyr Ser Gly Asp Ile
 115 120 125
 Arg Gln Leu Pro Arg Ala Glu Tyr Lys Pro Glu Lys Leu Pro Ser His
 130 135 140
 Ser Phe Glu Ile Asp His Glu Asp Ala Asp Lys Asp Glu Asp Thr Thr
 145 150 155 160
 Ser His Ser Ser Ser Lys Gly Gly Gly Gly Ala Gly Gly Thr Gly Val
 165 170 175
 Phe Lys Ser Gly Trp Leu Tyr Lys Gly Asn Phe Asn Ser Thr Val Asn
 180 185 190
 Asn Thr Val Thr Val Arg Ser Phe Lys Lys Arg Tyr Phe Gln Leu Thr
 195 200 205
 Gln Leu Pro Asp Asn Ser Tyr Ile Met Asn Phe Tyr Lys Asp Glu Lys
 210 215 220
 Ile Ser Lys Glu Pro Lys Gly Cys Ile Phe Leu Asp Ser Cys Thr Gly
 225 230 235 240
 Val Val Gln Asn Asn Arg Leu Arg Lys Tyr Ala Phe Glu Leu Lys Met
 245 250 255
 Asn Asp Leu Thr Tyr Phe Val Leu Ala Ala Glu Thr Glu Ser Asp Met
 260 265 270
 Asp Glu Trp Ile His Thr Leu Asn Arg Ile Leu Gln Ile Ser Pro Glu
 275 280 285
 Gly Pro Leu Gln Gly Arg Arg Ser Thr Glu Leu Thr Asp Leu Gly Leu
 290 295 300
 Asp Ser Leu Asp Asn Ser Val Thr Cys Glu Cys Thr Pro Glu Glu Thr
 305 310 315 320
 Asp Ser Ser Glu Asn Asn Leu His Ala Asp Phe Ala Lys Tyr Leu Thr
 325 330 335
 Glu Thr Glu Asp Thr Val Lys Thr Thr Arg Asn Met Glu Arg Leu Asn

a2b
 conf.

340					345					350					
Leu	Phe	Ser	Leu	Asp	Pro	Asp	Ile	Asp	Thr	Leu	Lys	Leu	Gln	Lys	Lys
		355					360					365			
Asp	Leu	Leu	Glu	Pro	Glu	Ser	Val	Ile	Lys	Pro	Phe	Glu	Glu	Lys	Ala
	370					375					380				
Ala	Lys	Arg	Ile	Met	Ile	Ile	Cys	Lys	Ala	Leu	Asn	Ser	Asn	Leu	Gln
	385					390					395				400
Gly	Cys	Val	Thr	Glu	Asn	Glu	Asn	Asp	Pro	Ile	Thr	Asn	Ile	Glu	Pro
				405					410					415	
Phe	Phe	Val	Ser	Val	Ala	Leu	Tyr	Asp	Leu	Arg	Asp	Ser	Arg	Lys	Ile
			420					425					430		
Ser	Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Ala	Ala	Val	Arg	Gln	Met
		435					440						445		
Leu	Leu	Gly	Ala	Ser	Val	Ala	Leu	Glu	Asn	Gly	Asn	Ile	Asp	Thr	Ile
	450					455					460				
Thr	Pro	Arg	Gln	Ser	Glu	Glu	Pro	His	Ile	Lys	Gly	Leu	Pro	Glu	Glu
	465					470					475				480
Trp	Leu	Lys	Phe	Pro	Lys	Gln	Ala	Val	Phe	Ser	Val	Ser	Asn	Pro	His
				485					490					495	
Ser	Glu	Ile	Val	Leu	Val	Ala	Lys	Ile	Glu	Lys	Val	Leu	Met	Gly	Asn
			500					505					510		
Ile	Ala	Ser	Gly	Ala	Glu	Pro	Tyr	Ile	Lys	Asn	Pro	Asp	Ser	Asn	Lys
		515					520					525			
Tyr	Ala	Gln	Lys	Ile	Leu	Lys	Ser	Asn	Arg	Gln	Phe	Cys	Ser	Lys	Leu
	530					535					540				
Gly	Lys	Tyr	Arg	Arg	Ala	Phe	Ala	Trp	Ala	Val	Arg	Ser	Val	Phe	Lys
	545					550					555				560
Asp	Asn	Gln	Gly	Asn	Val	Asp	Arg	Asp	Ser	Arg	Phe	Ser	Pro	Leu	Phe
				565					570					575	
Arg	Gln	Glu	Ser	Ser	Lys	Ile	Ser	Thr	Glu	Asp	Leu	Val	Lys	Leu	Val
			580					585					590		
Ser	Asp	Tyr	Arg	Arg	Ala	Asp	Arg	Ile	Ser	Lys	Met	Gln	Thr	Ile	Pro
		595					600					605			
Gly	Ser	Leu	Asp	Ile	Ala	Val	Asp	Asn	Val	Pro	Leu	Glu	His	Pro	Asn
	610					615					620				
Cys	Val	Thr	Ser	Ser	Phe	Ile	Pro	Val	Lys	Pro	Phe	Asn	Met	Met	Ala
	625					630					635				640
Gln	Thr	Glu	Pro	Thr	Val	Glu	Val	Glu	Glu	Phe	Val	Tyr	Asp	Ser	Thr
				645					650					655	
Lys	Tyr	Cys	Arg	Pro	Tyr	Arg	Val	Tyr	Lys	Asn	Gln	Ile	Tyr	Ile	Tyr
			660					665					670		

Q26
unt

Pro Lys His Leu Lys Tyr Asp Ser Gln Lys Cys Phe Asn Lys Ala Arg
 675 680 685
 Asn Ile Thr Val Cys Ile Glu Phe Lys Asn Ser Asp Glu Glu Ser Ala
 690 695 700
 Lys Pro Leu Lys Cys Ile Tyr Gly Lys Pro Glu Gly Pro Leu Phe Thr
 705 710 715 720
 Ser Ala Ala Tyr Thr Ala Val Leu His His Ser Gln Asn Pro Asp Phe
 725 730 735
 Ser Asp Glu Val Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His
 740 745 750
 His Ile Leu Phe Ser Phe Tyr His Val Thr Cys Asp Ile Asn Ala Lys
 755 760 765
 Ala Asn Ala Lys Lys Lys Glu Ala Leu Glu Thr Ser Val Gly Tyr Ala
 770 775 780
 Trp Leu Pro Leu Met Lys His Asp Gln Ile Ala Ser Gln Glu Tyr Asn
 785 790 795 800
 Ile Pro Ile Ala Thr Ser Leu Pro Pro Asn Tyr Leu Ser Phe Gln Asp
 805 810 815
 Ser Ala Ser Gly Lys His Gly Gly Ser Asp Ile Lys Trp Val Asp Gly
 820 825 830
 Gly Lys Pro Leu Phe Lys Val Ser Thr Phe Val Val Ser Thr Val Asn
 835 840 845
 Thr Gln Asp Pro His Val Asn Ala Phe Phe Gln Glu Cys Gln Lys Arg
 850 855 860
 Glu Lys Asp Met Ser Gln Ser Pro Thr Ser Asn Phe Ile Arg Ser Cys
 865 870 875 880
 Lys Asn Leu Leu Asn Val Glu Lys Ile His Ala Ile Met Ser Phe Leu
 885 890 895
 Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val Gln Asn Glu Glu
 900 905 910
 Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro Asp Ile Val Ala
 915 920 925
 Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln Ser Tyr Ile Lys
 930 935 940
 Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro Val His Glu Asp
 945 950 955 960
 Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn Asp Ser Pro Thr
 965 970 975
 Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe Ala Ile Ile Leu
 980 985 990

926
 cont.

Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys Ile Gln Leu Pro
 995 1000 1005
 Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu Leu Asp Asn Leu
 1010 1015 1020
 Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr Lys Asp Ala Leu
 1025 1030 1035 1040
 Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg Phe Leu Lys Arg
 1045 1050 1055
 Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys Met Val Asn Asn
 1060 1065 1070
 Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr Leu Cys Gln Tyr
 1075 1080 1085
 Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu His Phe Ile Pro
 1090 1095 1100
 Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp Pro Leu Thr Pro
 1105 1110 1115 1120
 Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met Pro Glu Tyr Ser
 1125 1130 1135
 Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile Gly Ile Leu Leu
 1140 1145 1150
 Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp Val Arg His Leu
 1155 1160 1165
 Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His Ser Phe Asp Asp
 1170 1175 1180
 Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met
 1185 1190 1195 1200
 Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg Ile Tyr Leu Lys
 1205 1210 1215
 Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln Gly Ser Arg Asp
 1220 1225 1230
 Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr Ala Ile Lys His
 1235 1240 1245
 Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val Leu Asn Ser Ile
 1250 1255 1260
 Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn His Ala Asp Ser
 1265 1270 1275 1280
 Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser Thr Asn Glu Lys
 1285 1290 1295
 Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro Arg Pro Leu Ala
 1300 1305 1310
 Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp Gln Ala Glu Thr

076
 cont.

1315	1320	1325
Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys Thr Ile Ser Tyr 1330	1335	1340
Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser Pro Glu Val Ser 1345	1350	1355 1360
Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn Phe Arg Tyr Leu 1365	1370	1375
Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala Phe Lys Phe Val 1380	1385	1390
Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser Asn Pro Ser Cys 1395	1400	1405
Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His 1410	1415	1420
Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro Ile Ile Arg Gly 1425	1430	1435 1440
Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr 1445	1450	1455
Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His His Val Asp Thr 1460	1465	1470
Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile Leu Asp Leu Val 1475	1480	1485
Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln Gln Cys Asp Cys 1490	1495	1500
Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr Met Leu Phe Phe 1505	1510	1515 1520
Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val Phe Ala Ser Leu 1525	1530	1535
Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe Gln Gly Pro Ala 1540	1545	1550
Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys Cys Cys Asn His 1555	1560	1565
Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu Leu Tyr Leu Phe 1570	1575	1580
Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser Ile Val Arg Ser 1585	1590	1595 1600
His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile Ala Asp Ala Gly 1605	1610	1615
Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile Thr Asn Asn Phe 1620	1625	1630
Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe Pro Ala Glu Val 1635	1640	1645

Q26
cont.

Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
 1650 1655 1660
 Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
 1665 1670 1675 1680
 Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu Arg Arg Thr Trp
 1685 1690 1695
 Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly Asp Leu Ser Glu
 1700 1705 1710
 Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu
 1715 1720 1725
 Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys Thr Ala Ser Leu
 1730 1735 1740
 Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser Leu Leu Thr Thr
 1745 1750 1755 1760
 Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro Ala Phe Leu Ser
 1765 1770 1775
 Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys Glu Asp Ser Gly
 1780 1785 1790
 Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr
 1795 1800 1805
 Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Leu Ile Ala
 1810 1815 1820
 Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe
 1825 1830 1835 1840
 Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys
 1845 1850 1855
 Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe Gly Arg Tyr Tyr
 1860 1865 1870
 Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly Lys
 1875 1880 1885
 Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser
 1890 1895 1900
 Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val
 1905 1910 1915 1920
 Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro
 1925 1930 1935
 Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu
 1940 1945 1950
 Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile
 1955 1960 1965

26
 end.

Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His
1970 1975 1980

Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser
1985 1990 1995 2000

His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val Ile Ser Gln Ser
2005 2010 2015

Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Arg
2020 2025 2030

Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met
2035 2040 2045

Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn
2050 2055 2060

Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala
2065 2070 2075 2080

Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg
2085 2090 2095

Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu
2100 2105 2110

Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr
2115 2120 2125

Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn Glu Gln Ile Thr
2130 2135 2140

Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln Thr Cys Thr Arg
2145 2150 2155 2160

Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val Ser Ile Ser Ser
2165 2170 2175

Ser Ala Glu Val
2180

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<400> 140
aggccttgtc tctgtttacc tg

22

<210> 141
<211> 23
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<400> 141
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23

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<400> 142
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19

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<400> 143
tatgtctcag tcacctacct g

21

<210> 144
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antisense primer

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24

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26

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Primer

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28

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cord.